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OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:45 ; Search time 12.9581 Seconds
(without alignments)
1524.850 Million cell updates/sec

Title: US-09-488-265B-29
Perfect score: 2462
Sequence: 1 MGVEVLLSLATLFGSTSGT.....DFVEGLSFARSGGNWAECA 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCRTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2408	97.8	467	4	US-09-273-871A-9
2	2282	92.7	441	3	US-09-121-425-1
3	2282	92.7	441	4	US-09-634-493A-1
4	2270	92.2	467	3	US-09-121-425-2
5	2270	92.2	467	4	US-09-634-493A-2
6	1879	76.3	467	1	US-07-923-724-8
7	1879	76.3	467	2	US-08-609-426A-8
8	1879	76.3	467	2	US-08-374-652C-2
9	1875	76.2	467	1	US-08-151-574-32
10	1875	76.2	467	1	US-08-146-424-20
11	1875	76.2	467	1	US-08-693-709-2
12	1875	76.2	467	2	US-08-419-448-32
13	1875	76.2	467	2	US-08-819-825-3
14	1875	76.2	467	3	US-09-163-642-3
15	1875	76.2	467	3	US-09-233-510-32
16	1875	76.2	467	4	US-09-636-499-5
17	1867	75.8	465	3	US-08-868-435-33
18	1867	75.8	465	4	US-08-744-211-33
19	1867	75.8	465	4	US-09-044-718-78
20	1867	75.8	465	4	US-09-636-499-6
21	1867	75.8	465	4	US-09-273-871A-8
22	1863	75.7	467	4	US-09-273-871A-11
23	1860	75.5	467	3	US-09-155-855-3
24	1860	75.5	467	4	US-09-543-744-3
25	1860	75.5	467	4	US-09-929-060-3
26	1859	75.5	465	4	US-09-044-718-80
27	1858	75.5	465	4	US-09-044-718-79

28	1857.5	75.4	439	4	US-09-044-718-3	Sequence 3, Appli
29	1857.5	75.4	449	4	US-09-044-718-12	Sequence 12, Appl
30	1855	75.3	465	4	US-09-044-718-81	Sequence 81, Appl
31	1851	75.2	462	4	US-09-636-499-12	Sequence 12, Appl
32	1845	74.9	469	4	US-09-044-718-82	Sequence 82, Appl
33	1839	74.7	466	3	US-08-868-435-35	Sequence 35, Appl
34	1839	74.7	466	4	US-08-744-231-35	Sequence 35, Appl
35	1835.5	74.6	463	3	US-08-868-435-29	Sequence 29, Appl
36	1835.5	74.6	463	4	US-08-744-231-29	Sequence 29, Appl
37	1835.5	74.6	463	4	US-09-273-871A-10	Sequence 10, Appl
38	1833	74.6	444	4	US-09-044-718-1	Sequence 1, Appli
39	1820.5	73.9	447	4	US-09-044-718-6	Sequence 6, Appli
40	1818	73.8	443	3	US-09-155-855-1	Sequence 1, Appli
41	1818	73.8	443	4	US-09-543-744-1	Sequence 1, Appli
42	1818	73.8	443	4	US-09-929-060-1	Sequence 1, Appli
43	1813	73.6	443	3	US-09-155-855-2	Sequence 2, Appli
44	1813	73.6	443	4	US-09-543-744-2	Sequence 2, Appli
45	1813	73.6	443	4	US-09-929-060-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-273-871A-9
; Sequence 9, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00606
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-09-273-871A-9

Query Match	97.8%	Score	2408	DB	4	Length	467
Best Local Similarity	97.9%	Pred. No.	1.9e-243				
Matches	457	Conservative	3	Mismatches	7	Indels	0
Gaps	0						
Qy	1	MGVEVLLSLATLFGSTSGTALGPRGNHSCDTVDGGYQCFPEISHLWGTYSFYFSLADE	60				
Db	1	MGVEVLLSLATLFGSTSGTALGPRGNHSCDTVDGGYQCFPEISHLWGTYSFYFSLADE	60				
Qy	61	SATSPDVPDDCRVTFVQVLSRHGARYPTSSAKAYSALIEAOKNATAFKGYAFUKTYN	120				
Db	61	SATSPDVPDDCRVTFVQVLSRHGARYPTSSAKAYSALIEAOKNATAFKGYAFUKTYN	120				
Qy	121	YTLGADDLTPFGENQMVNSGKIFYRYKALARKIVPFIRASGSDRVIAENKFIQFQSA	180				
Db	121	YTLGADDLTPFGENQMVNSGKIFYRYKALARKIVPFIRASGSDRVIAENKFIQFQSA	180				
Qy	181	KLADPGSQPHASPVINVIPEGSGYNNLTLDHGTCTAFDESELGDDVEANFTALFAPAIR	240				
Db	181	KLADPGSQPHASPVINVIPEGSGYNNLTLDHGTCTAFDESELGDDVEANFTALFAPAIR	240				

Db 181 KLADPGSOPHOASPVINDVTPEBSGYNNTLDHCTCTAFEDSHLGGDDVEANFTALFAPAIR 240
QY 241 ARLEADLPVGLTDEVDVYLMDMCPDFTVARTSDATLSPECALFTHDEWIOYDYLQSLG 300
|||||
Db 241 ARLEADLPVGLTDEVDVYLMDMCPETVARTSDATLSPECALFTHDEWIOYDYLQSLG 300
QY 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVDHTSTNHTLDSNPATFPLNATLYAFDS 360
|||||
Db 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVDHTSTNHTLDSNPATFPLNATLYAFDS 360
QY 361 HDNWTMISIFALGLYNGTKPLSTTSVESIETDGYASWTVPFAARAYVEMMOQAEKEP 420
|||||
Db 361 HDNWTMISIFALGLYNGTKPLSTTSVESIETDGYASWTVPFAARAYVEMMOQAEKEP 420
QY 421 LVRVLVNDVRVPLHGCAVDKLGCRKDDFVEGLSFARSGGNWAECEFA 467
|||||
Db 421 LVRVLVNDVRVPLHGCAVDKLGCRKDDFVEGLSFARSGGNWAECEFA 467
RESULT 2
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121.425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
US-09-121-425-1
Query Match 92.7%; Score 2282; DB 3; Length 441;
Best Local Similarity 97.7%; Pred. No. 2.8e-230;
Matches 431; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 27 NSHSCDVTDDGGYQCFPEISHLWCTYSPYFSLADESALSPDVPDCCRVTFVQVLSRHGARY 86
|||
Db 1 NSHSCDVTDDGGYQCFPEISHLWGOYSPYFSLADESALSPDVPDCCRVTFVQVLSRHGARY 60
|||
QY 87 PTSSASKAYSALIEAIOKNATAFKGYAFLKTYNTLTGADDLTPFGENOMVNSGKIFYRR 146
|||
Db 61 PTSSASKAYSALIEAIOKNATAFKGYAFLKTYNTLTGADDLTPFGENOMVNSGKIFYRR 120
|||
QY 147 YKALARKIVPFIRASGSDRVIASAEKFTIEGFQSAKLADPGSQPHOASPVINVIPEGSGY 206
|||
Db 121 YKALARKIVPFIRASGSDRVIASAEKFTIEGFQSAKLADPGSQPHOASPVIDVIPEGSGY 180
|||
QY 207 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRLEADLPGVTLTDEDVYVLMDCPF 266
|||
Db 181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRLEADLPGVTLTDEDVYVLMDCPF 240
|||
QY 267 DTVAKTSDATELSPFCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 326
|||
Db 241 EIVARTSDATELSPFCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 300
|||
QY 327 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSV 386
|||
Db 301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSV 360
|||
QY 387 ESIEETDGYASWTVPFAARAYVEMMOQAEKEPLVRVLVNDVRVPLHGCAVDKLGCRKR 446
|||
Db 361 ESIEETDGYASWTVPFAARAYVEMMOQAEKEPLVRVLVNDVRVPLHGCAVDKLGCRKR 420
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RESULT 4
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:

QY 447 DDFVEGLSFARSGGNWAECEFA 467
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Db 421 DDFVEGLSFARSGGNWAECEFA 441
RESULT 3
US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: Consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634.493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121.425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
US-09-634-493A-1
Query Match 92.7%; Score 2282; DB 4; Length 441;
Best Local Similarity 97.7%; Pred. No. 2.8e-230;
Matches 431; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
QY 27 NSHSCDVTDDGGYQCFPEISHLWCTYSPYFSLADESALSPDVPDCCRVTFVQVLSRHGARY 86
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Db 1 NSHSCDVTDDGGYQCFPEISHLWGOYSPYFSLADESALSPDVPDCCRVTFVQVLSRHGARY 60
|||||
QY 87 PTSSASKAYSALIEAIOKNATAFKGYAFLKTYNTLTGADDLTPFGENOMVNSGKIFYRR 146
|||||
Db 61 PTSSASKAYSALIEAIOKNATAFKGYAFLKTYNTLTGADDLTPFGENOMVNSGKIFYRR 120
|||||
QY 147 YKALARKIVPFIRASGSDRVIASAEKFTIEGFQSAKLADPGSQPHOASPVINVIPEGSGY 206
|||||
Db 121 YKALARKIVPFIRASGSDRVIASAEKFTIEGFQSAKLADPGSQPHOASPVIDVIPEGSGY 180
|||||
QY 207 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRLEADLPGVTLTDEDVYVLMDCPF 266
|||||
Db 181 NNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRLEADLPGVTLTDEDVYVLMDCPF 240
|||||
QY 267 DTVAKTSDATELSPFCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 326
|||||
Db 241 EIVARTSDATELSPFCALFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGFANELIAR 300
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QY 327 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSV 386
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Db 301 LTRSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSV 360
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QY 387 ESIEETDGYASWTVPFAARAYVEMMOQAEKEPLVRVLVNDVRVPLHGCAVDKLGCRKR 446
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Db 361 ESIEETDGYASWTVPFAARAYVEMMOQAEKEPLVRVLVNDVRVPLHGCAVDKLGCRKR 420
|||||
QY 447 DDFVEGLSFARSGGNWAECEFA 467
|||||
Db 421 DDFVEGLSFARSGGNWAECEFA 441

APPLICANT: Lehmann, Martin
TITLE OF INVENTION: Consensus Phytases
FILE REFERENCE: Consensus Phytases 13239
CURRENT APPLICATION NUMBER: US/09/121.425
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: EPO 97112688.3
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 467
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: consensus
OTHER INFORMATION: sequence
US-09-121-425-2

Query Match 92.2%; Score 2270; DB 3; Length 467;
Best Local Similarity 89.7%; Pred. No. 5.5e-229;
Matches 437; Conservative 3; Mismatches 7; Indels 40; Gaps 2;

QY 1 MGVFVLLSIATLFGSTSGTALGPRGNHSCDVTDDGGYQCFPEISHLWGTSPYFSLADE 60
DB 1 MGVFVLLSIATLFGSTSGTALGPRGNHSCDVTDDGGYQCFPEISHLWGTSPYFSLADE 60
QY 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
DB 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
QY 121 YTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 180
DB 101 YTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 160
QY 181 KLADPGSQPHQASPVIN-----VIIPEGSGYNNLTLDHGCTAFED 220
DB 161 KLADPGSQPHQASPVIDLIEAIQKNATAFKGYAFLKVIIPFEGSGYNNLTLDHGCTAFED 220
QY 221 SELGDDVEANFTALFAPAIRARLEADLPVTLTDEDVYVLMDCPFDVARTSDATELSP 280
DB 221 SELGDDVEANFTALFAPAIRARLEADLPVTLTDEDVYVLMDCPFDVARTSDATELSP 280
QY 281 FCALFTHDEWQYDYLSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNH 340
DB 281 FCALFTHDEWQYDYLSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNH 340
QY 341 TLDSNPATPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASWT 400
DB 341 TLDSNPATPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASWT 400
QY 401 VPFAARAYVEMMQCAEKEPLVRVLVNDVRVPLHGCAVDKLGCRKRDDEFVGLSFARSGG 460
DB 401 VPFAARAYVEMMQCAEKEPLVRVLVNDVRVPLHGCAVDKLGCRKRDDEFVGLSFARSGG 460
QY 461 NNAECFA 467
DB 461 NNAECFA 467

RESULT 5
US-09-634-493A-2
Sequence 2, Application US/09/634493A
Patent No. 6579975
GENERAL INFORMATION:
APPLICANT: Lehmann, Martin
TITLE OF INVENTION: Consensus Phytases
FILE REFERENCE: Consensus Phytases 13239
CURRENT APPLICATION NUMBER: US/09/634,493A
CURRENT FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: US/09/121.425
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: EPO 97112688.3
PRIOR FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 467
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: consensus
OTHER INFORMATION: sequence
US-09-634-493A-2

Query Match 92.2%; Score 2270; DB 4; Length 467;
Best Local Similarity 89.7%; Pred. No. 5.5e-229;
Matches 437; Conservative 3; Mismatches 7; Indels 40; Gaps 2;

QY 1 MGVFVLLSIATLFGSTSGTALGPRGNHSCDVTDDGGYQCFPEISHLWGTSPYFSLADE 60
DB 1 MGVFVLLSIATLFGSTSGTALGPRGNHSCDVTDDGGYQCFPEISHLWGTSPYFSLADE 60
QY 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
DB 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
QY 121 YTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 180
DB 101 YTLGADDLTPFGENQMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFIQFQSA 160
QY 181 KLADPGSQPHQASPVIN-----VIIPEGSGYNNLTLDHGCTAFED 220
DB 161 KLADPGSQPHQASPVIDLIEAIQKNATAFKGYAFLKVIIPFEGSGYNNLTLDHGCTAFED 220
QY 221 SELGDDVEANFTALFAPAIRARLEADLPVTLTDEDVYVLMDCPFDVARTSDATELSP 280
DB 221 SELGDDVEANFTALFAPAIRARLEADLPVTLTDEDVYVLMDCPFDVARTSDATELSP 280
QY 281 FCALFTHDEWQYDYLSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNH 340
DB 281 FCALFTHDEWQYDYLSLGKYYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNH 340
QY 341 TLDSNPATPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASWT 400
DB 341 TLDSNPATPLNATLYADFSHDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASWT 400
QY 401 VPFAARAYVEMMQCAEKEPLVRVLVNDVRVPLHGCAVDKLGCRKRDDEFVGLSFARSGG 460
DB 401 VPFAARAYVEMMQCAEKEPLVRVLVNDVRVPLHGCAVDKLGCRKRDDEFVGLSFARSGG 460
QY 461 NNAECFA 467
DB 461 NNAECFA 467

RESULT 6
US-09-923-724-8
Sequence 8, Application US/07923724
Patent No. 5780292
GENERAL INFORMATION:
APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m, Richard B.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington

STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Cimbala, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0240004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-923-724-8

Query Match 76.3%, Score 1879; DB 1: Length 467;
Best Local Similarity 75.6%, Pred. No. 5.1e-186;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVSFVLLSVATLFGSTGALPRGNSHSCDVTVDGGYQCFPEISHLWGTYSFYFSLADE 60
DB 1 MGVSFVLLSVATLFGSTGALPRGNSHSCDVTVDGGYQCFPEISHLWGTYSFYFSLADE 60

QY 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEIAOKNATAPFKGYAFLKTYN 120
DB 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEIAOKNATAPFKGYAFLKTYN 120

QY 121 YTLGADDLTPFGENOMVNSGKIFVRYKALARKIVPFIASGSDRVIASAEKFIEGFOSA 180
DB 121 YTLGADDLTPFGENOMVNSGKIFVRYKALARKIVPFIASGSDRVIASAEKFIEGFOSA 180

QY 181 KLADPGSOPHOASPVINVIIEGSGYNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
DB 181 KLADPGSOPHOASPVINVIIEGSGYNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240

QY 241 ARLEADLPGLTDEDVYVLMDCPDTVARTSDATFSLFPCALFTHDEWIQDYLOSIG 300
DB 241 ARLEADLPGLTDEDVYVLMDCPDTVARTSDATFSLFPCALFTHDEWIQDYLOSIG 300

QY 301 KYGCGAGNPLGPAQGVGFANELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADES 360
DB 301 KYGCGAGNPLGPAQGVGFANELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADES 360

QY 361 HDNMTISIFFALGYNKTLSTTSVSEIETOGYSASWTVPFAARAYVEMQOAEKEP 420
DB 361 HDNMTISIFFALGYNKTLSTTSVSEIETOGYSASWTVPFAARAYVEMQOAEKEP 420

QY 421 LVRVLNDRVPLHGCVAVDKGRCKRDDFVEGLSFAESGNGWAECA 467
DB 421 LVRVLNDRVPLHGCVAVDKGRCKRDDFVEGLSFAESGNGWAECA 467

RESULT 7
US-09-603-426A-8
Sequence 8, Application US/08609426A
Patent No. 5830733
GENERAL INFORMATION:
APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerström, Richard B.
TITLE OF INVENTION: Production of Phytase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,426A
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Grant E.
REGISTRATION NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 1050.0080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-609-426A-8

Query Match 76.3%, Score 1879; DB 2: Length 467;
Best Local Similarity 75.6%, Pred. No. 5.1e-186;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVSFVLLSVATLFGSTGALPRGNSHSCDVTVDGGYQCFPEISHLWGTYSFYFSLADE 60
DB 1 MGVSFVLLSVATLFGSTGALPRGNSHSCDVTVDGGYQCFPEISHLWGTYSFYFSLADE 60

QY 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEIAOKNATAPFKGYAFLKTYN 120
DB 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEIAOKNATAPFKGYAFLKTYN 120

Qy	121	YTLGADDLTPGEMQWNSGKFFRRYKALANKIVPFI	RASGSDRVIAAEKFI	EGFSQA	180
Db	121	YSLGADDLTPGEGELNSGKIFYRYEYSTRNIIPI	RSSGSSRVIAEGEKFI	EGFQST	180
Qy	181	KLADPGSOPHOASPINVIVPEGSYGYNLTLDHGTCTAFEDSELGDODVEANFTALFAPAIR	240		
Db	181	KLKDPRAQPGOSSPKIDVISEASSNNTLDPCCTVFEDSELADIVENFTATFAPSIR	240		
Qy	241	ARLEADLPGVLTIDEDVVYLMQMGPPOTVARTSDATELSPFCA	LFTHDEWIOQYDLOSLG	300	
Db	241	QRLNDELDSGVLTIDETVYLYMDMGSPDTISTSTVDTKLSPFCDLFTHDEWIHYDLOSLK	300		
Qy	301	KYGYGACGNPLGPAQGVGFANELIARLTHSPVODHTSTNHTLDSNPATPPLNAILYADEFS	360		
Db	301	KYYGHGACNPLGTPQGVGYANELIARLTHSPVHDDTSSNHTLDSNPATPPLNSTLYADEFS	360		
Qy	361	HDNTWISITFALGLYNGTKPLSTTSVSISIEETDGYSA	SWTPFAARAYVEMMQCAKEP	420	
Db	361	HDNGIISITLFGALYNGTKPLSTTTVENITQTQGFSSAWTPFASLYVEMMQCAQEP	420		
Qy	421	LYRVILVNDRVVPLHGCAVDKLGCRKRODFEGLSFARS	GGNWAECFA	467	
Db	421	LYRVILVNDRVVPLHGCPTIDALGRCTRDSFYRGLSFARS	GGDMAECSA	467	

RESULT 8

US-08-374-652C-2
: Sequence 2, Application US/08374652C
: Patent No. 5834286
: GENERAL INFORMATION:
: APPLICANT: NEVALAINEN, HELENA K.M.
: APPLICANT: PALOHEIMO, MARJA T.
: APPLICANT: FAGERSTROM, RICHARD B.
: APPLICANT: MIETTINEN-OINONEN, ARJA S.
: APPLICANT: TURUNEN, MARJA K.
: APPLICANT: RAMBOSEK, JOHN A.
: APPLICANT: PIDDINGTON, CHRISTOPHER S.
: APPLICANT: HOUSTON, CHRISTINE S.
: APPLICANT: CANIRELL, MICHAEL A.
: TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
: TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
: TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
: NUMBER OF SEQUENCES: 94
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
: STREET: 1100 NEW YORK AVENUE, SUITE 600
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/374.652C
: FILING DATE: 24-MAY-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/07058
: FILING DATE: 27-JUL-1993
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/925,401
: FILING DATE: 31-JUL-1992
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: REED, GRANT E.
: REGISTRATION NUMBER: 41,264
: REFERENCE/DOCKET NUMBER: 1050.071001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600

/	TELEFAX:	202-371-2540
/	INFORMATION FOR SEQ ID NO:	2:
/	SEQUENCE CHARACTERISTICS:	
/	LENGTH:	467 amino acids
/	TYPE:	amino acid
/	STRANDEDNESS:	single
/	TOPOLOGY:	not relevant
/	MOLECULE TYPE:	protein
/	US-08-374-652C-2	

	Query Match	76.3%	Score 1879;	DB 2:	Length 467;
	Best Local Similarity	75.6%	Pred. No. 5 le-188;		
	Matches 533;	Conservative 41;	Mismatches 73;	Indels	Gaps 0;
QY	1	MGVFVLLSIATLFGSTSGTALGPRNSHSCDTVDGGYOCFPFEISHLMGTWTSPIYSFLADE	60		
Db	1	: : : : : :			
QY	1	MGVSAVILLPYLLAGVTSGGLAVPASRNNQTCDITDVGQYCFSETSHLMGOYAPFFSLANE	60		
QY	61	SAISPDVPDCRVTFVOVLSSRHGARVPTSSAKAYSALIEAIOKNATAFKGYAFIAFKTYN	120		
Db	61	: : : : : :			
QY	121	YTLGADDLTPPGENQMVNSGIKYRYRKALARKIVPFIIRASGSORVIASAKKFTIEGFQSA	180		
Db	121	: : : : : : : :			
QY	181	KLAOPGSOPHOASPVINVIIPESGGYNNTLDHCTCTAREDSGLGDGVANETALFAPAIR	240		
Db	181	: : : : : : :			
QY	241	ARLEADLPGVTLTDDEVVYLMDMCPEDTVARTSDATELSPPCALFTHDEWIQDYQLASLG	300		
Db	241	: : : : : : :			
QY	301	KYYGYGAGNLGPQAQGVGFANELIARLIHSVPQDHSTWNHLDSNPATFPLNALIADFPS	360		
Db	301	: : : : : : :			
QY	361	HONTMISIFFEALGLNYNKGPKLSTTSVFSYEETDGYSASMTVPFAARAYVENMQCAKEP	420		
Db	361	: : : : : : :			
QY	421	JVRVLVNDRVVPLHGCAVDYKLGRCKRDDFVEGLSFARSGCNWAECFA	467		
Db	421	: : : : : : :			

RESULTS

US-08-151-574-32
Sequence 32, Application US/08151574
Patent No. 5436156
GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selten
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025-3471
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

```

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: SOFTWARE:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/151,574
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/688,578
: FILING DATE: 24-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H.
: REGISTRATION NUMBER: 25,959
: REFERENCE/DOCKET NUMBER: 24615-20026.00
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-327-7250
: INFORMATION FOR SEQ ID NO: 32:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 467 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-151-574-32

Query Match 75.28; Score 1875; DB 1; Length 467;
Best Local Similarity 75.68; Pred No. 1.3e-187;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLFGSTSGTALGPRGNHSCDVTGGYQCFFPEISHLMGTYSYFSLADE 60
DB 1 MGVSALLPLLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLMGQYAFPSLANE 60

QY 61 SAISPDPDCCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFKLTYN 120
DB 61 SVISPEVPAGCRVTFQVLSRHGARYPTDSKGYKYSALIEIQKNATTPDGKYAFKLTYN 120

QY 121 YTLGADDLTPFGENOMVNSGKIFRYRYKALARKIVPPIRASGSDRVIASAEKIEGFQSA 180
DB 121 YSLGADDLTPFGEQELVNSGKIFQRYESLTRNIVPPIRSGSSRVIASGKKIEGFQST 180

QY 181 KLADPGSQPHQASPVINVIIEPGSGYNTLDHGTCATFEDSELGDDVEANFTALFAPAIR 240
DB 181 KLKDPRAQPGQSPKIDVISEASSNNILDPGCTVFEDSELADTVEANFTATVPFSIR 240

QY 241 ARLEADLPGLVTLTDEDVYVLMDCPFDVTARTSDATELSPFCAFTHDEWIQYDYLQSLG 300
DB 241 QRLNDLSGVTLTDEVTYVLMDCSFDTISTVDTKLSPCDLFTHDEWINDYDYLQSLK 300

QY 301 KYYGAGNPLGPAQGVGFANELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
DB 301 KYYGAGNPLGPTQGVGYANELLARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

QY 361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMQCAKEP 420
DB 361 HDNGIISILFALGLYNGTKPLSTTIVENITQTDGFSSANTVPFASRLYVEMQCAKEP 420

QY 421 LVRVLNDRVPLHGCPCVDALGRCTRDSFVRGLSFARSGGDAECFA 467
DB 421 LVRVLNDRVPLHGCPCVDALGRCTRDSFVRGLSFARSGGDAECFA 467

RESULT 10
US-08-146-424-20
: Sequence 20, Application US/08/46424
: Patent No. 5593963
: GENERAL INFORMATION:
: APPLICANT: VAN OOIJEN, ALBERT J. J.
: APPLICANT: RIETVELD, KRIJN
: APPLICANT: HOEKEMA, ANDREAS
: APPLICANT: PEN, JAN
: APPLICANT: SIJMONS, PETER C.
: APPLICANT: VERWOERD, TEUNIS C.
: TITLE OF INVENTION: THE EXPRESSION OF PHYTASE IN PLANTS
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:

```

```

:
: ADDRESSEE: MORRISON & FOERSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/146,424
: FILING DATE: 02-NOV-1993
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: KENNEDY, BILL
: REGISTRATION NUMBER: 33,407
: REFERENCE/DOCKET NUMBER: 44615-20011.24
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: TELEX: 706141
: INFORMATION FOR SEQ ID NO: 20:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 467 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-146-424-20

Query Match 76.28; Score 1875; DB 1; Length 467;
Best Local Similarity 75.68; Pred No. 1.3e-187;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLFGSTSGTALGPRGNHSCDVTGGYQCFFPEISHLMGTYSYFSLADE 60
DB 1 MGVSALLPLLYLLSGVTSGLAVPASRNQSSCDTVDQGYQCFSETSHLMGQYAFPSLANE 60

QY 61 SAISPDPDCCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFKLTYN 120
DB 61 SVISPEVPAGCRVTFQVLSRHGARYPTDSKGYKYSALIEIQKNATTPDGKYAFKLTYN 120

QY 121 YTLGADDLTPFGENOMVNSGKIFRYRYKALARKIVPPIRASGSDRVIASAEKIEGFQSA 180
DB 121 YSLGADDLTPFGEQELVNSGKIFQRYESLTRNIVPPIRSGSSRVIASGKKIEGFQST 180

QY 181 KLADPGSQPHQASPVINVIIEPGSGYNTLDHGTCATFEDSELGDDVEANFTALFAPAIR 240
DB 181 KLKDPRAQPGQSPKIDVISEASSNNILDPGCTVFEDSELADTVEANFTATVPFSIR 240

QY 241 ARLEADLPGLVTLTDEDVYVLMDCPFDVTARTSDATELSPFCAFTHDEWIQYDYLQSLG 300
DB 241 QRLNDLSGVTLTDEVTYVLMDCSFDTISTVDTKLSPCDLFTHDEWINDYDYLQSLK 300

QY 301 KYYGAGNPLGPAQGVGFANELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
DB 301 KYYGAGNPLGPTQGVGYANELLARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360

QY 361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMQCAKEP 420
DB 361 HDNGIISILFALGLYNGTKPLSTTIVENITQTDGFSSANTVPFASRLYVEMQCAKEP 420

QY 421 LVRVLNDRVPLHGCPCVDALGRCTRDSFVRGLSFARSGGDAECFA 467
DB 421 LVRVLNDRVPLHGCPCVDALGRCTRDSFVRGLSFARSGGDAECFA 467

RESULT 11
US-08-693-709-2
: Sequence 2, Application US/08693709
: Patent No. 5770413
: GENERAL INFORMATION:

```

QY	301	KYYGAGNPLGPAQGVGANELIARLTHSPVQCHTSTNHTLDSNPATPLNATLYADFS	360
QY	301	KYYGAGNPLGPAQGVGANELIARLTHSPVQCHTSTNHTLDSNPATPLNATLYADFS	360
QY	361	HDNTMISIFALGLYNGTPLSTTSVESIEETDGTGYSASWTVPFAARAYVEMMQCAKEP	420
DB	361	HDNGIISILFALGLYNGTPLSTTSVESIEETDGTGYSASWTVPFAARAYVEMMQCAKEP	420
QY	421	LVRVLYNDRVVPLRGCAVDKLGKRCRDEVEGLSFARSGGMAECFA	467
DB	421	LVRVLYNDRVVPLRGCAVDKLGKRCRDEVEGLSFARSGGMAECFA	467

RESULT 12
US-08-419-448-32
Sequence 32, Application US/08419448
Patent No. 5863533
GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcum
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Seltin
TITLE OF INVENTION: Cloning and Expression of Microbial
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: JS/08/419,448
FILING DATE: 10-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-419-448-32

QY	1	MGVFFVLLSTATLFGSTGTALCPNGNSHSCDTPDGGYQCPEISHLWGTYSFVPSLADE	60
DB	1	MGVAVLLPLLYLLSGVTSGLAVPASRNQSCDTPDGGYQCPEISHLWGTYPFVPSLANE	60
QY	61	SAISPDVDDCRVTFVQVLSRHGARYPTSSAKYSALIEAIQKNATAFKGYAFKLTYN	120
DB	61	SVISPEVPACGRVTFVQVLSRHGARYPTSSAKYSALIEAIQKNATAFKGYAFKLTYN	120
QY	121	YTLGADDLTPFGENQMVNSGKIFRYRYKALAKIYFFIRAGSDRVIASAEKIEGQFSA	180
DB	121	YSLGADDLTPFGELVNSGKIFRYRYKALAKIYFFIRAGSDRVIASAEKIEGQFSA	180
QY	181	KLADPGSQPHASPVINVIIPGSGYNNLTDRGTCTAFEDSELGDDVEANFTALFAPAIR	240
DB	181	KLKDPRAQPGSQPKIDVVISSEASSNNTLDPGTCTVFEDSELADTVEANFTALFAPAIR	240
QY	241	ARLEADLPGLVTLDEVDVYLDMDCFDVTARTSDATELSPFCALTFHDEWYDYLQSLG	300
DB	241	ARLEADLPGLVTLDEVDVYLDMDCFDVTARTSDATELSPFCALTFHDEWYDYLQSLG	300

Query Match 76.2%; Score 1875; DB 1; Length 467;
Best Local Similarity 75.6%; Pred. No. 1.3e-187;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVFFVLLSTATLFGSTGTALCPNGNSHSCDTPDGGYQCPEISHLWGTYSFVPSLADE 60
DB 1 MGVAVLLPLLYLLSGVTSGLAVPASRNQSCDTPDGGYQCPEISHLWGTYPFVPSLANE 60
QY 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSAKYSALIEAIQKNATAFKGYAFKLTYN 120
DB 61 SVISPEVPACGRVTFVQVLSRHGARYPTSSAKYSALIEAIQKNATAFKGYAFKLTYN 120
QY 121 YTLGADDLTPFGENQMVNSGKIFRYRYKALAKIYFFIRAGSDRVIASAEKIEGQFSA 180
DB 121 YSLGADDLTPFGELVNSGKIFRYRYKALAKIYFFIRAGSDRVIASAEKIEGQFSA 180
QY 181 KLADPGSQPHASPVINVIIPGSGYNNLTDRGTCTAFEDSELGDDVEANFTALFAPAIR 240
DB 181 KLKDPRAQPGSQPKIDVVISSEASSNNTLDPGTCTVFEDSELADTVEANFTALFAPAIR 240
QY 241 ARLEADLPGLVTLDEVDVYLDMDCFDVTARTSDATELSPFCALTFHDEWYDYLQSLG 300
DB 241 ARLEADLPGLVTLDEVDVYLDMDCFDVTARTSDATELSPFCALTFHDEWYDYLQSLG 300

US-08-693-709-2

Query Match 76.2%; Score 1875; DB 1; Length 467;
Best Local Similarity 75.6%; Pred. No. 1.3e-187;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVFFVLLSTATLFGSTGTALCPNGNSHSCDTPDGGYQCPEISHLWGTYSFVPSLADE 60
DB 1 MGVAVLLPLLYLLSGVTSGLAVPASRNQSCDTPDGGYQCPEISHLWGTYPFVPSLANE 60
QY 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSAKYSALIEAIQKNATAFKGYAFKLTYN 120
DB 61 SVISPEVPACGRVTFVQVLSRHGARYPTSSAKYSALIEAIQKNATAFKGYAFKLTYN 120
QY 121 YTLGADDLTPFGENQMVNSGKIFRYRYKALAKIYFFIRAGSDRVIASAEKIEGQFSA 180
DB 121 YSLGADDLTPFGELVNSGKIFRYRYKALAKIYFFIRAGSDRVIASAEKIEGQFSA 180
QY 181 KLADPGSQPHASPVINVIIPGSGYNNLTDRGTCTAFEDSELGDDVEANFTALFAPAIR 240
DB 181 KLKDPRAQPGSQPKIDVVISSEASSNNTLDPGTCTVFEDSELADTVEANFTALFAPAIR 240
QY 241 ARLEADLPGLVTLDEVDVYLDMDCFDVTARTSDATELSPFCALTFHDEWYDYLQSLG 300
DB 241 ARLEADLPGLVTLDEVDVYLDMDCFDVTARTSDATELSPFCALTFHDEWYDYLQSLG 300

US-08-693-709-2

APPLICANT: VAN OIJEN, ALBERT J.J.
APPLICANT: R-ETVELD, KRIJN
APPLICANT: HOEKEMA, ANDREAS
APPLICANT: PEN, JAN
APPLICANT: SIJMONS, PETER C.
APPLICANT: VERWOERD, TEUNIS C.
TITLE OF INVENTION: THE EXPRESSION OF PHYTASE
TITLE OF INVENTION: IN PLANTS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/693,709
FILING DATE: 07-AUG-1996
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 08/146,424
FILING DATE: 02-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20011.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: Internal
FEATURE:
NAME/KEY: Signal Sequence
LOCATION: 1...23
OTHER INFORMATION:
US-08-693-709-2

Db 121 YSLGADDLTPFGEQELVNSGKIFQRYEISLRNIVPFIIRSSGSRVIASSKKFIEGFQST 180
QY 181 KLADPGSQPHQASPVINVIPECSGYNNLTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Db 181 KLKDPRAQPGQSPKIDVWISASSNNTLDPGTCTVFEDSELADTVEANFTAFVPSIR 240
QY 241 ARLEADLPVGLTDEVDVYLMDCMPDFTVARTSDATELSPFCALFTHDEWIQDYVLQSLG 300
Db 241 QRLNDLSGVLTDEVTYLMDCSFDTISTVDTKLSPPFCOLFTHDEWINDYVLQSLK 300
QY 301 KYGYGAGNPLGPAQGVGFANELLARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADF 360
Db 301 KYGYGAGNPLGPTQGVGVANELLARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADF 360
QY 361 HDNTMISIFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVENMCOCAKEP 420
Db 361 HDNGIISILFALGLYNGTKPLSTTIVENTQDGFSSAWTVPFASRLYVENMCOCAQEP 420
QY 421 LVRVLNDRVYPLHGCAVDKLGCRKRDDEVEGLSFARSGGNMAECFA 467
Db 421 LVRVLNDRVYPLHGCPVDALGRCRTDSEFVRLSFARSGGDMAECFA 467

RESULT 13

US-08-819-825-3
; Sequence 3, Application US/08819825
; Patent No. 5866118
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Ray, Michael W.
; APPLICANT: Klotz, Alan V.
; TITLE OF INVENTION: Polypeptides Having Phytase Activity
; TITLE OF INVENTION: And Nucleic Acids Encoding Same
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5866118 No. 5866118disk of No. 5866118th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 18-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4758-200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-819-825-3

Query Match 76.28; Score 1875; DB 2; Length 467;
Best Local Similarity 75.68; Pred. No. 1.3e-187;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;
QY 1 MGVEVLLSIATLFGSTSGTALGRGNHSCDVTGQYQCQFPEISHLWGTYSPVFLADP 60
Db 1 MGVSAYLLPYLLSGVTSLGLAVPASRNQSSCDIVDQYCFSETSHLWGQYAPFFFLANE 60

QY 61 SAISPDPDCCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFKLTYN 120
Db 51 SVISPEVPACGRVTPAQVLSRHGARYPTDSKGYKYSALIEIQONATTFDGKYAFKLTYN 120
QY 121 YTLGADDLTPFGEQELVNSGKIFQRYEISLRNIVPFIIRSSGSRVIASSKKFIEGFQST 180
Db 121 YSLGADDLTPFGEQELVNSGKIFQRYEISLRNIVPFIIRSSGSRVIASSKKFIEGFQST 180
QY 181 KLADPGSQPHQASPVINVIPECSGYNNLTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Db 181 KLKDPRAQPGQSPKIDVWISASSNNTLDPGTCTVFEDSELADTVEANFTAFVPSIR 240
QY 241 ARLEADLPVGLTDEVDVYLMDCMPDFTVARTSDATELSPFCALFTHDEWIQDYVLQSLG 300
Db 241 QRLNDLSGVLTDEVTYLMDCSFDTISTVDTKLSPPFCOLFTHDEWINDYVLQSLK 300
QY 301 KYGYGAGNPLGPAQGVGFANELLARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADF 360
Db 301 KYGYGAGNPLGPTQGVGVANELLARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADF 360
QY 361 HDNTMISIFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVENMCOCAKEP 420
Db 361 HDNGIISILFALGLYNGTKPLSTTIVENTQDGFSSAWTVPFASRLYVENMCOCAQEP 420
QY 421 LVRVLNDRVYPLHGCAVDKLGCRKRDDEVEGLSFARSGGNMAECFA 467
Db 421 LVRVLNDRVYPLHGCPVDALGRCRTDSEFVRLSFARSGGDMAECFA 467

RESULT 14

US-09-163-642-3
; Sequence 3, Application US/09163642
; Patent No. 6221644
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Ray, Michael W.
; APPLICANT: Klotz, Alan V.
; TITLE OF INVENTION: Polypeptides Having Phytase Activity
; TITLE OF INVENTION: And Nucleic Acids Encoding Same
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6221644 No. 6221644disk of No. 6221644th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 18-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J.
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4758-200-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 867 0123
; TELEFAX: 212 867 0298
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-163-642-3

Query Match 76.2%; Score 1875; DB 3; Length 467;
Best Local Similarity 75.6%; Pred. No. 1.3e-187;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVEVLLSIATLFGSTSGTALPGRNHSCDTPVGGYQCFPEISHLWGTYSYFSLADE 60
DB 1 MGVSALLPLLYLLSGVTSGLAVPASRNQSCDTPVGGYQCFSETSHLWQYAPFFSLANE 60

QY 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFLKTYN 120
DB 61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGYKYSALIEIOQNATTFDGKYAFLKTYN 120

QY 121 YTLGADDLTPFGENOMVNSGKIFRYRYKALARKIVPFIRASGSDRVIAAEKFIQFQSA 180
DB 121 YSLGADDLTPFGEOLVNSGKIFRYVESITRNIVPFIRSGSSRVIASGKKFIEGFQST 180

QY 181 KLADPGSOPHOASPVINVIPEGSGYNNITLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
DB 181 KLKDPRAQPGQSSPKIDWISEASSNNTLDPGCTVFEDSELADTVEANFTATFVPSIR 240

QY 241 ARLEADLPGLVLTDEDVYVLMDCPFDTVARTSDAIELSPFCALFTHDEMIOQDYLSLG 300
DB 241 ORLENDLSGVLTDEVTYVLMDCSFDTISTVVDIKLSPFCDLFTHDEWINKYLSL 300

QY 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
DB 301 KYGHGAGNPLGPTQGVYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

QY 361 HDNMTISIFFALGLYNGTKPLSTTSVESIEETDGYASMTVPFAARAYVEMMCOQAEKEP 420
DB 361 HDNGIISILFALGLYNGTKPLSTTTVENITQIDGFSSAWTVPFASRLYVEMMCOQAEQEP 420

QY 421 LVRVLVNDRVVPLHGCVAVDKLGCRKRDDEFGLSFARSGGNWAECEFA 467
DB 421 LVRVLVNDRVVPLHGCVPDAGLGRCTRDSFVRLGSLFARSGGDWAECEFA 467

RESULT 15

US-09-233-510-32
Sequence 32, Application US/09233510
Patent No. 6350602

GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Selzer
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025-3471

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE:

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233.510
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:

NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.00
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-233-510-32

Query Match 76.2%; Score 1875; DB 4; Length 467;
Best Local Similarity 75.6%; Pred. No. 1.3e-187;
Matches 353; Conservative 41; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVEVLLSIATLFGSTSGTALPGRNHSCDTPVGGYQCFPEISHLWGTYSYFSLADE 60
DB 1 MGVSALLPLLYLLSGVTSGLAVPASRNQSCDTPVGGYQCFSETSHLWQYAPFFSLANE 60

QY 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFLKTYN 120
DB 61 SVISPEVPAGCRVTFAQVLSRHGARYPTDSKGYKYSALIEIOQNATTFDGKYAFLKTYN 120

QY 121 YTLGADDLTPFGENOMVNSGKIFRYRYKALARKIVPFIRASGSDRVIAAEKFIQFQSA 180
DB 121 YSLGADDLTPFGEOLVNSGKIFRYVESITRNIVPFIRSGSSRVIASGKKFIEGFQST 180

QY 181 KLADPGSOPHOASPVINVIPEGSGYNNITLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
DB 181 KLKDPRAQPGQSSPKIDWISEASSNNTLDPGCTVFEDSELADTVEANFTATFVPSIR 240

QY 241 ARLEADLPGLVLTDEDVYVLMDCPFDTVARTSDAIELSPFCALFTHDEMIOQDYLSLG 300
DB 241 ORLENDLSGVLTDEVTYVLMDCSFDTISTVVDIKLSPFCDLFTHDEWINKYLSL 300

QY 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
DB 301 KYGHGAGNPLGPTQGVYANELIARLTHSPVHDDTSSNHTLDSSPATFPLNSTLYADFS 360

QY 361 HDNMTISIFFALGLYNGTKPLSTTSVESIEETDGYASMTVPFAARAYVEMMCOQAEKEP 420
DB 361 HDNGIISILFALGLYNGTKPLSTTTVENITQIDGFSSAWTVPFASRLYVEMMCOQAEQEP 420

QY 421 LVRVLVNDRVVPLHGCVAVDKLGCRKRDDEFGLSFARSGGNWAECEFA 467
DB 421 LVRVLVNDRVVPLHGCVPDAGLGRCTRDSFVRLGSLFARSGGDWAECEFA 467

Search completed: October 3, 2003, 07:47:49
Job time : 13.9581 secs

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OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:51 : Search time 106.714 Seconds
(without alignments)
692.370 Million cell updates/sec

Title: US-09-488-265B-29

Perfect score: 2462

Sequence: 1 MGVEVLLSLATLFGTSSTG.....DFVEGLSFARSGGNWAECPA 467

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/PCI_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*
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- 8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
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- 14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2408	97.8	467	14	US-10-083-452-9
2	1875	76.2	467	15	US-10-079-709-32
3	1875	76.2	467	15	US-10-229-358-5
4	1867	75.8	465	14	US-10-083-452-8
5	1867	75.8	465	15	US-10-062-848-78
6	1867	75.8	465	15	US-10-229-358-6
7	1863	75.7	467	14	US-10-083-452-11
8	1860.5	75.6	474	15	US-10-213-390-24
9	1860	75.5	467	9	US-09-929-060-3
10	1859	75.5	465	15	US-10-062-848-80
11	1858	75.5	465	15	US-10-052-848-79
12	1857.5	75.4	439	15	US-10-062-848-3
13	1857.5	75.4	449	15	US-10-062-848-12
14	1855	75.3	465	15	US-10-062-848-81
15	1851	75.2	462	15	US-10-229-358-12

16	1845	74.9	459	15	US-10-062-848-82
17	1835.5	74.6	463	14	US-10-083-452-10
18	1833	74.5	444	15	US-10-062-848-1
19	1820.5	73.9	447	15	US-10-062-848-6
20	1818	73.8	443	9	US-09-929-060-1
21	1813	73.6	443	9	US-09-929-060-2
22	1765	71.7	450	15	US-10-062-848-15
23	1761	71.5	466	14	US-10-083-452-12
24	1761	71.5	466	15	US-10-229-358-7
25	1719	69.8	466	14	US-10-083-452-13
26	1715.5	69.7	450	15	US-10-062-848-9
27	1714	69.6	438	15	US-10-062-848-2
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29	1627	66.1	489	15	US-10-229-358-10
30	1613	65.5	410	15	US-10-229-358-11
31	1334	54.2	475	14	US-10-083-452-14
32	1313.5	53.4	487	14	US-10-083-452-15
33	1313.5	53.4	487	15	US-10-229-358-8
34	1311	53.2	355	15	US-10-229-358-15
35	1187	48.2	495	14	US-10-083-452-2
36	1182	48.0	478	14	US-10-083-452-3
37	902	36.6	284	15	US-10-229-358-19
38	855	34.7	283	15	US-10-229-358-9
39	855	34.7	283	15	US-10-229-358-24
40	802.5	32.6	443	14	US-10-083-452-5
41	798.5	32.4	439	14	US-10-083-452-7
42	795.5	32.3	453	14	US-10-083-452-6
43	781	31.7	442	14	US-10-083-452-4
44	702.5	28.5	212	15	US-10-229-358-16
45	401	16.3	312	15	US-10-229-358-21

ALIGNMENTS

RESULT 1
US-10-083-452-9
: Sequence 9, Application US/10083452
: Publication No. US20020127218A1
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: TITLE OF INVENTION: Phytase Variants
: FILE REFERENCE: 5618.500-US
: CURRENT APPLICATION NUMBER: US/10/083,452
: CURRENT FILING DATE: 2002-02-26
: PRIOR APPLICATION NUMBER: US/09/273,871
: PRIOR FILING DATE: 1999-03-22
: PRIOR APPLICATION NUMBER: PA 1998 00407
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: PA 1998 00806
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: PA 1998 01176
: PRIOR FILING DATE: 1998-09-18
: PRIOR APPLICATION NUMBER: PA 1999 00091
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/080,129
: PRIOR FILING DATE: 1998-03-31
: PRIOR APPLICATION NUMBER: 60/090,675
: PRIOR FILING DATE: 1998-06-25
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 467
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Variation
US-10-083-452-9

Query Match 97.8%; Score 2408; DB 14; Length 467;
Best Local Similarity 97.9%; Pred. No. 4.1e-230;
Matches 457; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

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QY 1 MGCVFVLLSIATLFGSTSGTALGRGNHSCDVTGQYQCFPEISHLWGIYSYFSLADE 60
DB 1 MGCVFVLLSIATLFGSTSGTALGRGNHSCDVTGQYQCFPEISHLWGIYSYFSLADE 60
QY 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFLKTYN 120
DB 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFLKTYN 120
QY 121 YTLGADDLTPFGENOMVNSGTFKYYRYKALARKIVPPIRASGSDRVIASAEKIEGFQSA 180
DB 121 YTLGADDLTPFGENOMVNSGTFKYYRYKALARKIVPPIRASGSDRVIASAEKIEGFQSA 180
QY 181 KLADPGSOPHOASPVINVIPEGSGYNTIDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
DB 181 KLADPGSOPHOASPVINVIPEGSGYNTIDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
QY 241 ARLEADLPGVTLTDEDVYVLMDCPFDTVARTSDATELSPPCALFTHDEWYQDYIQLSLG 300
DB 241 ARLEADLPGVTLTDEDVYVLMDCPFDTVARTSDATELSPPCALFTHDEWYQDYIQLSLG 300
QY 301 KYGYGAGNPLGPAQGVGFANELLARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
DB 301 KYGYGAGNPLGPAQGVGFANELLARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
QY 361 HDNMTISIFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMMCOQAEKEP 420
DB 361 HDNMTISIFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMMCOQAEKEP 420
QY 421 LVRVLNDRVVPVPLHGCAYDKLGRCKRDDFVEGLSFARSGGNWAECEFA 467
DB 421 LVRVLNDRVVPVPLHGCAYDKLGRCKRDDFVEGLSFARSGGNWAECEFA 467
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RESULT 2

US-10-079-709-32

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; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; SOFTWARE: Patent in Release #1.0, Version #1.25
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-10-079-709-32
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Query Match 76.2%; Score 1875; DB 15; Length 467;

Best Local Similarity 75.6%; Pred. No. 3.4e-177; Indels 0; Gaps 0;

Matches 553; Conservative 41; Mismatches 73;

QY 1 MGCVFVLLSIATLFGSTSGTALGRGNHSCDVTGQYQCFPEISHLWGIYSYFSLADE 60

DB 1 MGCVFVLLSIATLFGSTSGTALGRGNHSCDVTGQYQCFPEISHLWGIYSYFSLADE 60

QY 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFLKTYN 120

DB 61 SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFLKTYN 120

QY 121 YTLGADDLTPFGENOMVNSGTFKYYRYKALARKIVPPIRASGSDRVIASAEKIEGFQSA 180

DB 121 YTLGADDLTPFGENOMVNSGTFKYYRYKALARKIVPPIRASGSDRVIASAEKIEGFQSA 180

QY 181 KLADPGSOPHOASPVINVIPEGSGYNTIDHGTCTAFEDSELGDDVEANFTALFAPAIR 240

DB 181 KLADPGSOPHOASPVINVIPEGSGYNTIDHGTCTAFEDSELGDDVEANFTALFAPAIR 240

QY 241 ARLEADLPGVTLTDEDVYVLMDCPFDTVARTSDATELSPPCALFTHDEWYQDYIQLSLG 300

DB 241 ARLEADLPGVTLTDEDVYVLMDCPFDTVARTSDATELSPPCALFTHDEWYQDYIQLSLG 300

QY 301 KYGYGAGNPLGPAQGVGFANELLARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360

DB 301 KYGYGAGNPLGPAQGVGFANELLARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360

QY 361 HDNMTISIFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMMCOQAEKEP 420

DB 361 HDNMTISIFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFAARAYVEMMCOQAEKEP 420

QY 421 LVRVLNDRVVPVPLHGCAYDKLGRCKRDDFVEGLSFARSGGNWAECEFA 467

DB 421 LVRVLNDRVVPVPLHGCAYDKLGRCKRDDFVEGLSFARSGGNWAECEFA 467

RESULT 3

US-10-229-358-5

; Sequence 5, Application US/10229358

; Publication No. US20030124700A1

; GENERAL INFORMATION:

; APPLICANT: Stafford, Christian F.

; APPLICANT: Trinci, Anthony P.J.

; APPLICANT: Brookman, Jayne L.

; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding

; FILE REFERENCE: GC586-2

; CURRENT APPLICATION NUMBER: US/10/229,358

; CURRENT FILING DATE: 2002-08-26

; PRIOR APPLICATION NUMBER: US 60/148,960

; PRIOR FILING DATE: 1999-08-13

; NUMBER OF SEQ ID NOS: 34

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5

; LENGTH: 467

; TYPE: PRI

; ORGANISM: Aspergillus niger

; US-10-229-358-5

Query Match 76.2%; Score 1875; DB 15; Length 467;

Best Local Similarity 75.6%; Pred. No. 3.4e-177;

QY 421 LVRVLNDKRVPLHGCADKVLGRCKRDDVEGLSFARSGGNNAECFA 467
DB 421 LVRVLNDKRVPLHGCADKVLGRCKRDDVEGLSFARSGGNNAECFA 467

RESULT 8

US-10-213-950-24
; Sequence 24, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
; FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213.990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-950-24

Query Match 75.6%; Score 1860.5; DB 15; Length 474;
Best Local Similarity 75.3%; Pred. No. 9.5e-176;
Matches 351; Conservative 41; Mismatches 67; Indels 7; Gaps 2;

QY 2 GVEVLLSIATLFGSTGTALGPRGNHSCDVTGCGYOCPEISHLWCTSPYPSLADES 61
DB 16 GAVVLKRSRVSAPSS-----AGSKSCDVTDLGQCSPATSHLWQYSPFFSLEDEL 69
QY 62 AISPDPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFELKTYN 121
DB 70 SVSSKLPKDCRITLQVLSRHGARYPTSSSKYKYLVAIQANATDFKGFALKTYN 125
QY 122 TLGADDLTPFGENOMVNSGKIFRYRYKALARKIVPFIRASGSDRVIASAEKPIEGFQSAK 181
DB 130 TLGADDLTPFGEOQLVNSGKIFRYRYKALARSVPVFFIRASGSDRVIASGEXKPIEGFQQAQ 189
QY 182 LADPGSOPHOASPVNIVTIPESGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIRA 241
DB 190 LADPGA-TNRAAPALSVLIPSEIFENNTLDHGVCTKFEASGDDVEANFTALFAPAIRA 248
QY 242 RLEADLPQVTLTDEDVYLMDCPFDIVARTSDATELSPPFCALFTHDEWIQDYLOSJGK 301
DB 249 RAEXHLPGVTLTDEDVYLMDCSFDIVARTSDASQLSPFCOLFTHNEWKYNYLQSLGK 308
QY 302 YGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHLSDSNPATFPLNATLYADF 361
DB 309 YGYGAGNPLGPAQGIPTNLCIARLTHSPVQDHTSTNHLSDSNPATFPLNATLYADF 368
QY 362 DNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASMTVPFAARAYVEMMCOCKEPL 421
DB 369 DNSWVSIFFALGLYNGTEPLSRTSVESAKELDGYASWVVPFGARAYFETNQCCKEPL 428
QY 422 VRLVNDKRVPLHGCADKVLGRCKRDDVEGLSFARSGGNNAECFA 467
DB 429 VRLVNDKRVPLHGCADKVLGRCKRDDVEGLSFARSGGNNAECFA 474

RESULT 9

US-09-929-060-3
; Sequence 3, Application US/09929060
; Patent No. US20020068350A1
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIDEWASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI

; APPLICANT: JANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/929.060
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-09-929-060-3

Query Match 75.5%; Score 1860; DB 9; Length 467;
Best Local Similarity 74.1%; Pred. No. 1e-175;
Matches 346; Conservative 48; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVEVLLSIATLFGSTGTALGPRGNHSCDVTGCGYOCPEISHLWCTSPYPSLADE 60
DB 1 MGVSALLPLLYLLSGVTSLGLAVPASRNRQSTCDIVDQGYOCFSETSHLWQYAPFFSLANK 6C
QY 61 SAISPDPDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFELKTYN 120
DB 61 SAISPDPVAGCHVTFAQVLSRHGARYPTDSKGGKYSALIEIQONATTFEGKYAFELKTYN 120
QY 121 YTLGADDLTPFGENOMVNSGKIFRYRYKALARKIVPFIRASGSDRVIASAEKPIEGFQSA 180
DB 121 YSLGADDLTPFGEOQLVNSGKIFRYRYKALARKIVPFIRASGSDRVIASGNKPIEGFQST 180
QY 181 KLADPGSOPHOASPVNIVTIPESGYNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
DB 181 KLADPRAQPCOSSPKIDVIVISEASTSNNTLDPGCTVFEDELADIEANFTATFVPSIR 240
QY 241 ARLEADLPQVTLTDEDVYLMDCPFDIVARTSDATELSPPFCALFTHDEWIQDYLOSJG 300
DB 241 QRLNLDLGGVSLTDEVTYLMDCSFDITSTVDTKLSPPCDFLTHEEWINDYLOSJN 300
QY 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHLSDSNPATFPLNATLYADE 360
DB 301 KYTGHGAGNPLGPIQGVGFANELIARLTHSPVHDDTSSNHLSDSNPATFPLNATLYADE 360
QY 361 HDNTMISIFFALGLYNGTKPLSTTSVESIEETDGYASMTVPFAARAYVEMMCOCKEPL 420
DB 361 HDNGIISILFALGLYNGTKPLSSTTAENITQTDGFSASMTVPFASRMVEMMCOCKEPL 420
QY 421 LVRVLNDKRVPLHGCADKVLGRCKRDDVEGLSFARSGGNNAECFA 467
DB 421 LVRVLNDKRVPLHGCADKVLGRCKRDDVEGLSFARSGGNNAECFA 467

RESULT 10

US-10-062-848-80
; Sequence 80, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062.848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 465
; TYPE: PR1
; ORGANISM: Aspergillus fumigatus
US-10-062-848-80

Query Match 75.5%; Score 1859; DB 15; Length 465;
Best Local Similarity 75.8%; Pred. No. 1.3e-175;
Matches 354; Conservative 36; Mismatches 75; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATIFGSGTALGPRGNHSCDVTVDGGYQCFPEISHLWGTYSYFSLADE 60
DB 1 MVTLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGQYSYFSLADE 59

QY 61 SAISPDPVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
DB 60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKYKLVTAIOANATDFKGFAPLKYN 119

QY 121 YTLGADDLTPGEGNOMVNSGKIFVRRYKALARKIVPIRASGSDRVIASAEKIEGFQSA 180
DB 120 YTLGADDLTPGEGQOLVNSGKIFQRYKALARSVVPPIRASGSDRVIASGEKIEGFQQA 179

QY 181 KLADPGSOPHOASPVINVIPEGSGYNNTLDHGCTAFEDSELGDDVEANFTALFAPAIR 240
DB 180 KLADPGA-TNRAAPAISVPIPESETFNNTLDHGCTKFEASQOLGDEVAANFTALFAPDIR 238

QY 241 ARLEADLPVLTDEDDVYVLMDCMCFDTVARTSDATLSLSPFCALFTHDEWIQDYLOSGL 300
DB 239 ARAEKHLPGVLTDEDDVYVLMDCMCFDTVARTSDASQLSPFCQLFTHNEWKYNYLOSGL 298

QY 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATMYVDFS 360
DB 299 KYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATMYVDFS 358

QY 361 HNTMISIFFALGLYNGTKPLSTTSVESIETDGYASWTVPPFAARAYVEMQCAKEP 420
DB 359 HNSMVSIFFFALGLYNGTEPLSRTSVESAKELDGYASWVVPFGARAYFETMOCKSEKES 418

QY 421 LVRVLNDRVPLHGCAVDKLGCRCKRDOFVEGLSFARSGGNWAECPA 467
DB 419 LVRALINDRVVPLHGCDVDKLGCRCKLNDFVKGLSWARSGGNWGECPFS 465

RESULT 11
US-10-062-848-79
; Sequence 79, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 465
; TYPE: PR1
; ORGANISM: Aspergillus fumigatus
US-10-062-848-79

Query Match 75.5%; Score 1858; DB 15; Length 465;
Best Local Similarity 75.8%; Pred. No. 1.6e-175;
Matches 354; Conservative 36; Mismatches 75; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATIFGSGTALGPRGNHSCDVTVDGGYQCFPEISHLWGTYSYFSLADE 60
DB 1 MVTLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGQYSYFSLADE 59

QY 61 SAISPDPVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
DB 60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKYKLVTAIOANATDFKGFAPLKYN 119

QY 121 YTLGADDLTPGEGNOMVNSGKIFVRRYKALARKIVPIRASGSDRVIASAEKIEGFQSA 180
DB 120 YTLGADDLTPGEGQOLVNSGKIFQRYKALARSVVPPIRASGSDRVIASGEKIEGFQQA 179

QY 181 KLADPGSOPHOASPVINVIPEGSGYNNTLDHGCTAFEDSELGDDVEANFTALFAPAIR 240
DB 180 KLADPGA-TNRAAPAISVPIPESETFNNTLDHGCTKFEASQOLGDEVAANFTALFAPDIR 238

QY 241 ARLEADLPVLTDEDDVYVLMDCMCFDTVARTSDATLSLSPFCALFTHDEWIQDYLOSGL 300
DB 239 ARAEKHLPGVLTDEDDVYVLMDCMCFDTVARTSDASQLSPFCQLFTHNEWKYNYLOSGL 298

QY 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADES 360
DB 299 KYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATMYVDFS 358

QY 361 HNTMISIFFALGLYNGTKPLSTTSVESIETDGYASWTVPPFAARAYVEMQCAKEP 420
DB 359 HNSMVSIFFFALGLYNGTEPLSRTSVESAKELDGYASWVVPFGARAYFETMOCKSEKES 418

QY 421 LVRVLNDRVPLHGCAVDKLGCRCKRDOFVEGLSFARSGGNWAECPA 467
DB 419 LVRALINDRVVPLHGCDVDKLGCRCKLNDFVKGLSWARSGGNWGECPFS 465

RESULT 12
US-10-062-848-3
; Sequence 3, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 439
; TYPE: PR1
; ORGANISM: Aspergillus fumigatus
US-10-062-848-3

Query Match 75.4%; Score 1857.5; DB 15; Length 439;
Best Local Similarity 78.9%; Pred. No. 1.7e-175;
Matches 347; Conservative 36; Mismatches 56; Indels 1; Gaps 1;

QY 28 SHSCDVTVDGGYQCFPEISHLWGTYSYFSLADESAISPDVDDCRVTFVQVLSRHGARYP 87
DB 1 SKSCDVTDLGYQCSPATSHLWGQYSYFSLADELSVSSKLPKDCRITLVQVLSRHGARYP 60

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QY 88 TSSASKAYSALIEAIQKNATAFKGYAFELKTYNTYTLGADDLI?PFGENQMVNSGZKFTYRY 147
DB 61 ISSKSKYKLVTAIOANATDFKGFAPFLKTYNTYTLGADDLI?PFGQQQVNSGKFTYRY 120
QY 148 KALARKIVDFIRASSSDRVIAAEKFIQFQSAKLADPGSQPHQASPVINVIIPGSGYN 207
DB 121 KALARSVVPFIRASSSDRVIAASGEKFIQFQSAKLADPGCA-TNRAAPALSVIIPSEIFN 179
QY 208 NTLDHGCTCFADSELDGDOVEANFTALFAPAIRARLEADLPQVTLTDEDVYVLMQCPFD 267
DB 180 NTLDHGCVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVYVLMQCSFD 239
QY 268 TVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFANELIARL 327
DB 240 TVARTSDASQLSPFCOLFTHNEWKKNYLYQSLGKYGYGAGNPLGPAQGIQFTNELIARL 299
QY 328 THSPVODHTSTNHTLDSNPATPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTSVE 387
DB 300 TRSPVODHTSTNHTLDSNPATPLNATLYADFSDHNSWVSJFFALGLYNGTEPLSRISVE 359
QY 388 SIETDGYASMTVPFAARAYVEMMOCAKEPLVRLVNDRVVPLHGCADVKGCRKRD 447
DB 360 SAKELDGYASWVYPGARAYFETMOCKSEKPEPLVRALINDRVVPLHGCADVKGCRKLN 419
QY 448 DFVEGLSFARSGGNWAECEFA 467
DB 420 DFVKGLSWARSGGNWGECEFS 439

RESULT 13
US-10-062-848-12
; Sequence 12, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.5
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-12

Query Match 75.4%; Score 1857.5; DB 15; Length 449;
Best Local Similarity 78.9%; Pred. No. 1-7e-175;
Matches 347; Conservative 36; Mismatches 56; Indels 1; Gaps 1;

QY 28 SHSCDVTGQYQCFEISHLWGTYSYFSLADESAISPDVDDCRVTFVQVLSRHGARYP 87
DB 11 SKSCDVTDLGQCSPATSHLWGOYSPFSELEDSVSKLPKDCRITLTVQVLSRHGARYP 70
QY 88 TSSASKAYSALIEAIQKNATAFKGYAFELKTYNTYTLGADDLI?PFGENQMVNSGKFTYRY 147
DB 71 TSSKSKYKLVTAIOANATDFKGFAPFLKTYNTYTLGADDLI?PFGQQQVNSGKFTYRY 130
QY 148 KALARKIVDFIRASSSDRVIAAEKFIQFQSAKLADPGSQPHQASPVINVIIPGSGYN 207
DB 131 KALARSVVPFIRASSSDRVIAASGEKFIQFQSAKLADPGCA-TNRAAPALSVIIPSEIFN 189
QY 208 NTLDHGCTCFADSELDGDOVEANFTALFAPAIRARLEADLPQVTLTDEDVYVLMQCPFD 267
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DB 190 NTLDHGCVCTKFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVYVLMQCSFD 249
QY 268 TVARTSDATELSPFCALFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFANELIARL 327
DB 250 TVARTSDASQLSPFCOLFTHNEWKKNYLYQSLGKYGYGAGNPLGPAQGIQFTNELIARL 309
QY 328 THSPVODHTSTNHTLDSNPATPLNATLYADFSDHNTMISIFFALGLYNGTKPLSTTSVE 387
DB 310 TRSPVODHTSTNHTLDSNPATPLNATLYADFSDHNSWVSJFFALGLYNGTEPLSRISVE 369
QY 388 SIETDGYASMTVPFAARAYVEMMOCAKEPLVRLVNDRVVPLHGCADVKGCRKRD 447
DB 370 SAKELDGYASWVYPGARAYFETMOCKSEKPEPLVRALINDRVVPLHGCADVKGCRKLN 429
QY 448 DFVEGLSFARSGGNWAECEFA 467
DB 430 DFVKGLSWARSGGNWGECEFS 449

RESULT 14
US-10-062-848-81
; Sequence 81, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.5
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Query Match 75.3%; Score 1855; DB 15; Length 465;
Best Local Similarity 75.6%; Pred. No. 3.2e-175;
Matches 353; Conservative 37; Mismatches 75; Indels 2; Gaps 2;

QY 1 MGVEVVVLSIATLFGSTSGTALGPRGNHSCDVTGQYQCFEISHLWGTYSYFSLADE 60
DB 1 MVTTLTFLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGQCSPATSHLWGOYSPFSELE 59
QY 61 SAISPDPVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFELKTYN 120
DB 60 LSVSSKLPKDCRITLTVQVLSRHGARYPTSSKSKYKLVTAIOANATDFKGFAPFLKTYN 119
QY 121 YTLGADDLI?PFGENQMVNSGKFTYRYKALARKIVDFIRASSSDRVIAAEKFIQFQSA 180
DB 120 YTLGADDLI?PFGQQQVNSGKFTYRYKALARSVVPFIRASSSDRVIAASGEKFIQFQSA 179
QY 181 KLADPGSQPHQASPVINVIIPGSGYNNTLDHGTCTAFEDSELGDOVEANFTALFAPAIR 240
DB 180 KLADPGCA-TNRAAPALSVIIPSEIFNNTLDHGTCTAFEDSELGDOVEANFTALFAPAIR 238
QY 241 ARLEADLPQVTLTDEDVYVLMQCPFDVTARTSDATELSPFCALFTHDEWIQYDYLQSLG 300
DB 239 ARAKHLPGVTLTDEDVYVLMQCSFDVTARTSDASQLSPFCOLFTHNEWKKNYLYQSLG 298
QY 301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVODHTSTNHTLDSNPATPLNATLYADF 360
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Db      299 KYGYGAGNPLGPAQIGICTNELIARLTRSPVQDHTSTNSTLVSNPATFPLNATMYDFS 358
Qy      361 HDNTMISIFFALGYNGTKPLSTISVSIESIETDGYSSASHTVPFAARAYVEMMQOAEKEP 420
Db      359 HDNSWVSIFFAALGYNGTEPLSRSTVSASAKELDYSASWVYPGARAYFETMOCKSEKEP 418
Qy      421 LVRVLNDRVPLHGCAVDKLGCRKRDDFEVGLSFARSGGNWAECEFA 467
Db      419 LVRALINDRVVPLHGCDVDKLGCRCKLNDKLVKGLSWARSGGNWGECEFS 465

RESULT 15
US-10-229-358-12
; Sequence 12, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-229-358-12

Query Match      75.2%      Score 1851: DB:15: Length 462:
Best Local Similarity 75.5%: Pred. No. 8e-175:
Matches 349: Conservative 41: Mismatches 72: Indels 0: Gaps 0:

Qy      1  MGVEVLLSIATLFGSTGALGPRGNSHSDTVDGYQCFPEISHLWGTYSVPYFLADE 60
Db      1  MGVSALLPLLYLLSGVTSLAVPASRNOSSCDTVDOGYQCFSETHLWGYAPFESLANE 60
Qy      61  SAISPDVDDCRVTFVQVLSRHGARYPTSSASKAYSALIEAIQKNATAFKGYAFLKTYN 120
Db      61  SWISPEVPAGCRVTFQAQVLSRHGARYPTDSKGYKYSALIEEIQONATTFDGKYAFLKTYN 120
Qy      121 YTLGADDLTPFGENOMVNSGKIFYRRYKALARKIVPFIASGSDRVIASAEKFTIEGFOSA 180
Db      121 YSLGADDLTPFGELVNSGKIFYRYESLFTNIVYFIRSSGSRVITASGKKFIEGFQST 180
Qy      181 KLADPGSQPHQASPVINVIIPGSGYNNTLDHGCTAFEDSELGDDVEANETALFAPAIR 240
Db      181 KLADPRAQPGQSSPKIDVYSEASSNNTLDPGCTVFEDSELADTVEANFTATFAPSIR 240
Qy      241 ARLEADLPGVTLTDEDVYVLDMPCPDVTARTSDATELSPFCALFTHDEWIDYDYLQSLG 300
Db      241 QRLNDLSGVTLTDEVTYVLDMPCSFDLTISTVDTKLSPCDFLTHDEWINIDYLSLK 300
Qy      301 KYGYGAGNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db      301 KYGYHGAGNPLGPTQGVGVANELIARLTHSPVHDDTSSNHTLDSNPATFPLNSTLYADFS 360
Qy      361 HDNTMISIFFALCYNGTKPLSTISVESIEETDGYSSASHTVPFAARAYVEMMQOAEKEP 420
Db      361 HDNGIISILFALGYNGTKPLSTTTTVENITQTDGFSSAWTVPFASRLYVEMMQOAEKEP 420
Qy      421 LVRVLNDRVPLHGCAVDKLGCRKRDDFEVGLSFARSGGNW 462
Db      421 LVRVLNDRVPLHGCFVDALGCRTRDSFVRLGSLFARSGDW 462
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Search completed: October 3, 2003, 08:12:30
Job time : 107.714 secs

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OM protein - protein search, using sw model

Run On: October 3, 2003, 07:46:51 ; Search time 106.774 Seconds
(without alignments)
692.370 Million cell updates/sec

Title: US-09-488-265B-31

Perfect score: 2468

Sequence: 1 MGVFVLLSLATLFGSTGT.....DFVEGLSFARSGGNWEBCFA 467

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, AA:*

1: /cgn2_6/ptodata1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2308	93.5	467	14	US-10-083-452-9
2	1888	76.5	465	14	US-10-083-452-8
3	1888	76.5	465	15	US-10-062-848-78
4	1888	76.5	465	15	US-10-229-358-6
5	1881.5	76.2	474	15	US-10-213-990-24
6	1880	76.2	465	15	US-10-062-848-80
7	1879	76.1	465	15	US-10-062-848-79
8	1878.5	76.1	439	15	US-10-062-848-3
9	1878.5	76.1	449	15	US-10-062-848-12
10	1876	76.0	465	15	US-10-062-848-81
11	1854	75.1	469	15	US-10-062-848-82
12	1848	74.9	467	15	US-10-079-709-32
13	1848	74.9	467	15	US-10-229-358-5
14	1841	74.6	467	9	US-09-929-060-3
15	1836	74.4	467	14	US-10-083-452-11

16	1829	74.1	462	15	US-10-229-358-12
17	1806	73.2	444	15	US-10-062-848-1
18	1804.5	73.1	463	14	US-10-083-452-10
19	1799	72.9	443	9	US-09-929-060-1
20	1794	72.7	443	9	US-09-929-060-2
21	1789.5	72.5	447	15	US-10-062-848-6
22	1752	71.0	466	14	US-10-083-452-12
23	1752	71.0	466	15	US-10-229-358-7
24	1748	70.8	450	15	US-10-062-848-15
25	1710	69.3	466	14	US-10-083-452-13
26	1706.5	69.1	450	15	US-10-062-848-9
27	1697	68.6	438	15	US-10-062-848-2
28	1658	67.2	489	15	US-10-229-358-4
29	1658	67.2	489	15	US-10-229-358-10
30	1623	65.8	410	15	US-10-229-358-11
31	1381	56.0	475	14	US-10-083-452-14
32	1339	54.3	355	15	US-10-229-358-15
33	1334.5	54.1	487	14	US-10-083-452-15
34	1334.5	54.1	487	15	US-10-229-358-8
35	1215	49.2	495	14	US-10-083-452-2
36	1210	49.0	478	14	US-10-083-452-3
37	920	37.3	284	15	US-10-229-358-19
38	867	35.1	283	15	US-10-229-358-9
39	867	35.1	283	15	US-10-229-358-24
40	845.5	34.3	443	14	US-10-083-452-5
41	833.5	33.8	453	14	US-10-083-452-6
42	830.5	33.7	439	14	US-10-083-452-7
43	825	33.4	442	14	US-10-083-452-4
44	729.5	29.6	212	15	US-10-229-358-16
45	406	16.5	312	15	US-10-229-358-21

ALIGNMENTS

RESULT 1

US-10-083-452-9
; Sequence 9, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083.452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273.871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 004C7
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080.129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090.675
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-10-083-452-9

Query Match 93.5%; Score 2308; DB 14; Length 467;
Best Local Similarity 93.4%; Pred. No. 6.9e-224;
Matches 436; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

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QY 1 MGVFVLLSIATLPGSTGCTALGPRGNHSCDVTVDGGYQCPEISHLWGTYSPPFSLADE 60
Db 1 MGVFVLLSIATLPGSTGCTALGPRGNHSCDVTVDGGYQCPEISHLWGTYSPPFSLADE 60
QY 61 SAISPDVPKGCRTVTVQVLSRHGARYPTSSKASKAYSALIEAIQKNATAFKGYAFLKTYN 120
Db 61 SAISPDVPKGCRTVTVQVLSRHGARYPTSSKASKAYSALIEAIQKNATAFKGYAFLKTYN 120
QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFTIEGFOSA 180
Db 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFTIEGFOSA 180
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
QY 241 ARLEAHLPGVNTLDEVDVNLMDMCPFDVARTSDATQSPFCDLFTHDENQYDYLOSGL 300
Db 241 ARLEAHLPGVNTLDEVDVNLMDMCPFDVARTSDATQSPFCDLFTHDENQYDYLOSGL 300
QY 301 KYGYGAGNPLGPAOGVGFVNELIARLTHSPVQDHTSTNNHILDSNPATFPLNATLYADF 360
Db 301 KYGYGAGNPLGPAOGVGFVNELIARLTHSPVQDHTSTNNHILDSNPATFPLNATLYADF 360
QY 361 HNTMYSIFFALGLYNGTKPLSTTSVESIEETDGYASASWTVPFAARAYVENMCOQAEKEP 420
Db 361 HNTMYSIFFALGLYNGTKPLSTTSVESIEETDGYASASWTVPFAARAYVENMCOQAEKEP 420
QY 421 LVRVLNDRVPLHGGGVGDKLGRCKRDDFVEGLSFARSGGNWEECEFA 467
Db 421 LVRVLNDRVPLHGGGVGDKLGRCKRDDFVEGLSFARSGGNWEECEFA 467
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RESULT 2

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US-10-083-452-8
; Sequence 8, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-083-452-8
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Query Match 76.5%; Score 1888; DB 14; Length 465;
Best Local Similarity 76.9%; Pred. No. 1.6e-181;
Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;
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QY 1 MGVFVLLSIATLPGSTGCTALGPRGNHSCDVTVDGGYQCPEISHLWGTYSPPFSLADE 60
Db 1 MGVFVLLSIATLPGSTGCTALGPRGNHSCDVTVDGGYQCPEISHLWGTYSPPFSLADE 60
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QY 61 SAISPDVPKGCRTVTVQVLSRHGARYPTSSKASKAYSALIEAIQKNATAFKGYAFLKTYN 120
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QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFTIEGFOSA 180
Db 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFTIEGFOSA 180
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
QY 241 ARLEAHLPGVNTLDEVDVNLMDMCPFDVARTSDATQSPFCDLFTHDENQYDYLOSGL 300
Db 241 ARLEAHLPGVNTLDEVDVNLMDMCPFDVARTSDATQSPFCDLFTHDENQYDYLOSGL 300
QY 301 KYGYGAGNPLGPAOGVGFVNELIARLTHSPVQDHTSTNNHILDSNPATFPLNATLYADF 360
Db 301 KYGYGAGNPLGPAOGVGFVNELIARLTHSPVQDHTSTNNHILDSNPATFPLNATLYADF 360
QY 361 HNTMYSIFFALGLYNGTKPLSTTSVESIEETDGYASASWTVPFAARAYVENMCOQAEKEP 420
Db 361 HNTMYSIFFALGLYNGTKPLSTTSVESIEETDGYASASWTVPFAARAYVENMCOQAEKEP 420
QY 421 LVRVLNDRVPLHGGGVGDKLGRCKRDDFVEGLSFARSGGNWEECEFA 467
Db 421 LVRVLNDRVPLHGGGVGDKLGRCKRDDFVEGLSFARSGGNWEECEFA 467
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RESULT 3

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US-10-062-848-78
; Sequence 78, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-78
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Query Match 76.5%; Score 1888; DB 15; Length 465;
Best Local Similarity 76.9%; Pred. No. 1.6e-181;
Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;
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QY 1 MGVFVLLSIATLPGSTGCTALGPRGNHSCDVTVDGGYQCPEISHLWGTYSPPFSLADE 60
Db 1 MGVFVLLSIATLPGSTGCTALGPRGNHSCDVTVDGGYQCPEISHLWGTYSPPFSLADE 60
QY 61 SAISPDVPKGCRTVTVQVLSRHGARYPTSSKASKAYSALIEAIQKNATAFKGYAFLKTYN 120
Db 61 SAISPDVPKGCRTVTVQVLSRHGARYPTSSKASKAYSALIEAIQKNATAFKGYAFLKTYN 120
QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFTIEGFOSA 180
Db 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFIIRASGSDRVIASAEKFTIEGFOSA 180
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
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```
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-80

Query Match      76.2%; Score 1880; DB 15; Length 465;
Best Local Similarity 76.7%; Pred. No. 1.1e-180;
Matches 358; Conservative 35; Mismatches 72; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATLFGSTGTALGRGNHSCDITVDGGYQCFFPEISHLWGTYSPPFSLEADE 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MVTLTFLLSAAYLLSGRVSAAPSSAG -SKSCDVTDLGYQCSPATSHLWGOYSPFFSLEDE 59
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFKLTYN 120
   : : : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 60 LSVSKLPKDCRITLVQVLSRHGARYPTSSASKYKLVTAIOANATDFKGFALFKTYN 119
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFIRASGSDRVIASAEKIEGFQSA 180
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 120 YTLGADDLTPFGEQOLVNSGKIFQRYKALARSVVPFIRASGSDRVIASGEKIEGFQQA 179
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 181 KLAOPGANPHOASPVINVIPEGAGYNNITLDHGLCTAFESSELGDDVEANFTAVFAPPIR 240
   : : : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 180 KLAOPGAT -NRAAPSAISVIIPESETFNNTLDHGCTKFEASQLGDEVAANFTALFAPDIR 238
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 241 ARLEAHLPGVNLTDDEVVNLMDMCPEDTAVRTSDATQSPFCDLTFHDEWIQDYLOSGL 300
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 239 ARAEKHLPGVLTDEVVNLMDMCSFDTVARTSDASQLSPFCQLTFHNEWKYNYLQSLG 298
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 301 KYGYGAGNPLGPAOGVGVNELLARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADF 360
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 299 KYGYGAGNPLGPAOGIGFTNELIARLTHSPVQDHTSTNSTLVSNPATFPLNATMYVDF 358
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 361 HDNTWVSIFPFGALGYNGTKPLSTTSVESIETDGYASASWTVPFAARAYVENMOCEAKEP 420
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 359 HDNSWVSIFPFGALGYNGTEPLSRTSVESAKELDGYASASWVVPFGARAYFETMOCKSEK 418
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 421 LVRVLNDRVPLHCGVDKLGCRKRDQDFVEGLSFARSGGNWCECFA 467
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 419 LVRALINDRVVPLHGCDDVKLGCRCKLNDVFKGLSWARSGGNWGECEFS 465
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RESULT 7
US-10-062-848-79
; Sequence 79, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
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; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-79

Query Match      76.1%; Score 1879; DB 15; Length 465;
Best Local Similarity 76.7%; Pred. No. 1.3e-180;
Matches 358; Conservative 35; Mismatches 72; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATLFGSTGTALGRGNHSCDITVDGGYQCFFPEISHLWGTYSPPFSLEADE 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MVTLTFLLSAAYLLSGRVSAAPSSAG -SKSCDVTDLGYQCSPATSHLWGOYSPFFSLEDE 59
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFKLTYN 120
   : : : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 60 LSVSKLPKDCRITLVQVLSRHGARYPTSSASKYKLVTAIOANATDFKGFALFKTYN 119
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFIRASGSDRVIASAEKIEGFQSA 180
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 120 YTLGADDLTPFGEQOLVNSGKIFQRYKALARSVVPFIRASGSDRVIASGEKIEGFQQA 179
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 181 KLAOPGANPHOASPVINVIPEGAGYNNITLDHGLCTAFESSELGDDVEANFTAVFAPPIR 240
   : : : : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 180 KLAOPGAT -NRAAPSAISVIIPESETFNNTLDHGCTKFEASQLGDEVAANFTALFAPDIR 238
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 241 ARLEAHLPGVNLTDDEVVNLMDMCPEDTAVRTSDATQSPFCDLTFHDEWIQDYLOSGL 300
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 239 ARAEKHLPGVLTDEVVNLMDMCSFDTVARTSDASQLSPFCQLTFHNEWKYNYLQSLG 298
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 301 KYGYGAGNPLGPAOGVGVNELLARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADF 360
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 299 KYGYGAGNPLGPAOGIGFTNELIARLTHSPVQDHTSTNSTLVSNPATFPLNATMYVDF 358
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 361 HDNTWVSIFPFGALGYNGTKPLSTTSVESIETDGYASASWTVPFAARAYVENMOCEAKEP 420
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 359 HDNSWVSIFPFGALGYNGTEPLSRTSVESAKELDGYASASWVVPFGARAYFETMOCKSEK 418
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 421 LVRVLNDRVPLHCGVDKLGCRKRDQDFVEGLSFARSGGNWCECFA 467
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 419 LVRALINDRVVPLHGCDDVKLGCRCKLNDVFKGLSWARSGGNWGECEFS 465
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
US-10-062-848-3
; Sequence 3, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
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US-10-062-848-3

Query Match 76.1%; Score 1878.5; DB 15; Length 439;
Best Local Similarity 79.8%; Pred. No. 1.4e-180;
Matches 35; Conservative 35; Mismatches 53; Indels 1; Gaps 1;

QY 28 SHSCDTVDGGYOCFPEISHLMWYTSFFSFLADESAISPDVPGCRVTFVQVLSRHGARYP 87
DB 1 SKSCDTVDLGYCSPATSHLMWQYSPFFSFLADELSVSKLPKDCRITLVQVLSRHGARYP 60

QY 88 TSSASKAYSALIEAIOKNATAPFKGYAFKTYNTILGADDLTPFGQOVMVNSGKIFRYR 147
DB 61 TSSKSKYKKLVTAIQANATDFGKFAFLKTYNTILGADDLTPFGQOVMVNSGKIFRYR 120

QY 148 KALARKIVPPIRASGSDRVIASAEKFTIEGFSQAKLADPGANPHQASPVNIIPEGAGYN 207
DB 121 KALARSVVPPIRASGSDRVIASAEKFTIEGFSQAKLADPGAT-NRAAPASVIIPESEIEN 179

QY 208 NTLDHGLCTAFEESELGDVEANFTAVFAPPIRARLEAHLPGVNLTDVWNLMDMCPED 267
DB 190 NTLDHGCTVFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVWSLMDMCSFD 249

QY 268 TVARTSDATOLSPCCDLFTHEMIQDYLOSLOKYYGYGAGNPLGPAQGVGFVFNELIARL 327
DB 240 TVARTSDASQLSPCCDLFTHEMKYNYLOSLOKYYGYGAGNPLGPAQGVGFVFNELIARL 299

QY 328 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMYSIFFALGLYNGTKPLSTTSVE 387
DB 300 TRSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMYSIFFALGLYNGTKPLSTTSVE 359

QY 388 SIEETDGYASWTVPFAARAYVENMOCEAEKEPLRVLVNDRVVPVPLHGCDVDRGCK3D 447
DB 360 SAKELDGYASWVVPFGARAYFETMCKSEKEPLRVLRALINDRVVPLHGCDVDRGCK3D 419

QY 448 DFVEGLSFARSGGNWCEFA 467
DB 420 DFVKGLSWARSGGNWCEFS 439

RESULT 9
US-10-062-848-12
; Sequence 12, Application US/10062848
; Publication No. US2003092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-12

Query Match 76.1%; Score 1878.5; DB 15; Length 449;
Best Local Similarity 79.8%; Pred. No. 1.4e-180;
Matches 35; Conservative 35; Mismatches 53; Indels 1; Gaps 1;

QY 28 SHSCDTVDGGYOCFPEISHLMWYTSFFSFLADESAISPDVPGCRVTFVQVLSRHGARYP 87
DB 11 SKSCDTVDLGYCSPATSHLMWQYSPFFSFLADELSVSKLPKDCRITLVQVLSRHGARYP 70

QY 88 TSSASKAYSALIEAIOKNATAPFKGYAFKTYNTILGADDLTPFGQOVMVNSGKIFRYR 147
DB 71 TSSKSKYKKLVTAIQANATDFGKFAFLKTYNTILGADDLTPFGQOVMVNSGKIFRYR 130

QY 148 KALARKIVPPIRASGSDRVIASAEKFTIEGFSQAKLADPGANPHQASPVNIIPEGAGYN 207
DB 131 KALARSVVPPIRASGSDRVIASAEKFTIEGFSQAKLADPGAT-NRAAPASVIIPESEIEN 189

QY 208 NTLDHGLCTAFEESELGDVEANFTAVFAPPIRARLEAHLPGVNLTDVWNLMDMCPED 267
DB 190 NTLDHGCTVFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVWSLMDMCSFD 249

QY 268 TVARTSDATOLSPCCDLFTHEMIQDYLOSLOKYYGYGAGNPLGPAQGVGFVFNELIARL 327
DB 250 TVARTSDASQLSPCCDLFTHEMKYNYLOSLOKYYGYGAGNPLGPAQGVGFVFNELIARL 309

QY 328 THSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMYSIFFALGLYNGTKPLSTTSVE 387
DB 310 TRSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMYSIFFALGLYNGTKPLSTTSVE 369

QY 388 SIEETDGYASWTVPFAARAYVENMOCEAEKEPLRVLVNDRVVPVPLHGCDVDRGCK3D 447
DB 370 SAKELDGYASWVVPFGARAYFETMCKSEKEPLRVLRALINDRVVPLHGCDVDRGCK3D 429

QY 448 DFVEGLSFARSGGNWCEFA 467
DB 430 DFVKGLSWARSGGNWCEFS 449

RESULT 10
US-10-062-848-81
; Sequence 81, Application US/10062848
; Publication No. US2003092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Query Match 76.0%; Score 1876; DB 15; Length 465;
Best Local Similarity 76.4%; Pred. No. 2.7e-180;
Matches 35; Conservative 36; Mismatches 72; Indels 2; Gaps 2;

QY 1 MGVFVVLISLTIPLGSGTALGPRGNHSCDTPVGGYQCFPEISHLMWYTSFFSFLADE 60
DB 1 MVLTLFLLSAVLLSGRVSAAAPSSAG-SKSCDTVDLGYCSPATSHLMWQYSPFFSLEDE 59

QY 61 SAISPDVPGCRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAPFKGYAFKTYN 120
DB 60 LSVSKLPKDCRITLVQVLSRHGARYPTSSASKAYSALIEAIOKNATAPFKGYAFKTYN 119

QY 121 YTLGADDLTPFGQOVMVNSGKIFRYRKYKALARKIVPPIRASGSDRVIASAEKFTIEGFSQA 180
DB 120 YTLGADDLTPFGQOVMVNSGKIFRYRKYKALARSVVPPIRASGSDRVIASAEKFTIEGFSQA 179

QY 421 LVRVLVNDRVVPLHGGCVKDLGRCKRDFVEGLSFARSGGNWEECFA 467
Db 421 LVRVLVNDRVVPLHGGCVKDLGRCKRDFVEGLSFARSGGNWEECFA 467

Search completed: October 3, 2003, 08:12:32
Job time : 108.714 secs

RESULT 15
US-10-083-452-11
; Sequence 11, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus ficuum
US-10-083-452-11

Query Match 74.4%; Score 1836; DB 14; Length 467;
Best Local Similarity 73.9%; Pred. No. 2 9e-176;
Matches 345; Conservative 42; Mismatches 80; Indels 3; Gaps 0;
QY 1 MGVEVWILSTATLFGSTSTALGPRNSHSCDTPDGGYQCFPEISHLMGTYSPPFSLADE 60
Db 1 MGVSALLPLLYLLSGVTSLGAVPASRNQSCDTPDGGYQCFSETSHLMGQYAPFFSLANE 60
QY 61 SATSPDVKGCRVTFVQVLSRHGARYPTSSASKAYSALIEAQKNATAFKGYAFKTYN 120
Db 61 SVISPEVPACCRVTFPAQVLSRHGARYPTSDGKYSALIEEQNATTFDKGYAFKTYN 120
QY 121 YTLGADDLTPFGQOMVNSGKIFRYKALARKIVPFTIRASGSDRVIASAEKPIEGFOSA 180
Db 121 YSLGADDLTPFGQELVNSGKIFRYQYELRNIVPFIKSSGSRVIAAGKKFIEGFQST 180
QY 181 KLADPGANPHQASPVNVLIPGAGYNNLTLDHGLCTAFEESELGDDVEANFTAVFAPEIR 240
Db 181 KLKDPRAQCQSPKIDVILSEASSNNLTDPCTCTVFEDELADTVFANFTATVPVSIR 240
QY 241 ARLEAHLPGVNLTDVNLMDMCPDVTARTSQTLSFPCDFTDHEWYQYDYLQSLG 300
Db 241 ORLENDLSGVTLDTEVIVLMDMCSPTDITSTVDTKLSFFCDLFTDHEWYDYLQSLK 300
QY 301 KYGYGAGNPLGPAQGVFNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 360
Db 301 KYGHGAGNPLGPTQGVYANELIARLTHSPVHDDTSSNHTLDSNPATFPLKSTLYADFS 360
QY 361 HONTMVSIFFALGLYNGTKPLSTTSVESIEETDGYASWTVFAARAYVEMMQCEAKEP 420
Db 361 HDNGIISILFALGLYNGTKPLSTTTVENITQTDGESSANTVFFASRLYVENMQCEAQAP 420
QY 421 LVRVLVNDRVVPLHGGCVKDLGRCKRDFVEGLSFARSGGNWEECFA 467
Db 421 LVRVLVNDRVVPLHGGCVKDLGRCKRDFVEGLSFARSGGNWEECFA 467

Db 181 KLADPGSOPHCASPVIDVILPEGSGYNNLTLDHGTCTAFEDSELGDDVEANFTALFAPAK 240
Qy 241 ARLEAHLPGVNLTDDEVDVNLMDCPEDTIVARTSDATQLSPFCDLFTDHEWIDYDLSLG 300
Db 241 ARLEADLPVTLTDEDVYLMDMCPETIVARTSDATLSLSPFCALFTDHEWROYDYLSLG 300
Qy 301 KYGYGAGNPLGPAQGVFNELIARLTHSPVDHTSTNHTLDSNPATPLNATLYADPS 360
Db 301 KYGYGAGNPLGPAQGVFNELIARLTHSPVDHTSTNHTLDSNPATPLNATLYADPS 360
Qy 361 HDNPMWIFFALGLYNGTKPLSTTSVESIETDGYASMTVPFAARAYVEMMOCEAREP 420
Db 361 HDNPMWIFFALGLYNGTKPLSTTSVESIETDGYASMTVPFAARAYVEMMOCEAREP 420
Qy 421 LVRVLVNDVRVPLHGCGVCKLGRCKRDFVEGLSFARSGGNWEECEFA 467
Db 421 LVRVLVNDVRVPLHGCGVCKLGRCKRDFVEGLSFARSGGNWEECEFA 467

RESULT 2
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121.425
; PRIOR FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-121-425-1

Query Match 88.4%; Score 2182; DB 3; Length 441;
Best Local Similarity 93.0%; Pred. No. 1.le-216;
Matches 410; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

Qy 27 NSHSCDIVDGGYQCFFPEISHLWGTSPFFSLADESALSIPDKGCRVTFVQVLSRHGARY 86
Db 1 NSHSCDIVDGGYQCFFPEISHLWGTSPFFSLADESALSIPDKGCRVTFVQVLSRHGARY 60
Qy 87 PTSSASKAYSALIEAIOKNATAFKGYAFKTYNTILGADDLTPFGEQOMVNSGKIFERY 146
Db 61 PTSSASKAYSALIEAIOKNATAFKGYAFKTYNTILGADDLTPFGEQOMVNSGKIFERY 120
Qy 147 YKALARKIVPPIRAGSDRVIASAEKIEGFSQAKLADPGANPHQASPVINVIPEGAGY 206
Db 121 YKALARKIVPPIRAGSDRVIASAEKIEGFSQAKLADPGANPHQASPVINVIPEGAGY 180
Qy 207 NNTLDHGLCTAFEDSELGDDVEANFTALFAPARLEADLPVTLTDEDVYVLMDCPF 240
Db 181 NNTLDHGLCTAFEDSELGDDVEANFTALFAPARLEADLPVTLTDEDVYVLMDCPF 240
Qy 267 DTVARTSDATLSLSPFCALFTDHEWROYDYLSLGKYYGAGNPLGPAQGVFNELIAR 326
Db 241 DTVARTSDATLSLSPFCALFTDHEWROYDYLSLGKYYGAGNPLGPAQGVFNELIAR 300
Qy 327 LTHSPVDHTSTNHTLDSNPATPLNATLYADFSHDNTMYSIFFALGLYNGTKPLSTTSV 386
Db 301 LTRSPVDHTSTNHTLDSNPATPLNATLYADFSHDNTMYSIFFALGLYNGTKPLSTTSV 360
Qy 387 ESIEETDGYASMTVPFAARAYVEMMOCEAREKPELVRVLVNDVRVPLHGCGVCKLGRCKR 446
Db 361 ESIEETDGYASMTVPFAARAYVEMMOCEAREKPELVRVLVNDVRVPLHGCGVCKLGRCKR 420

Qy 447 DDFVEGLSFARSGGNWEECEFA 467
Db 421 DDFVEGLSFARSGGNWEECEFA 441

RESULT 3
US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634.493A
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121.425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-634-493A-1

Query Match 88.4%; Score 2182; DB 4; Length 441;
Best Local Similarity 93.0%; Pred. No. 1.le-216;
Matches 410; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

Qy 27 NSHSCDIVDGGYQCFFPEISHLWGTSPFFSLADESALSIPDKGCRVTFVQVLSRHGARY 86
Db 1 NSHSCDIVDGGYQCFFPEISHLWGTSPFFSLADESALSIPDKGCRVTFVQVLSRHGARY 60
Qy 87 PTSSASKAYSALIEAIOKNATAFKGYAFKTYNTILGADDLTPFGEQOMVNSGKIFERY 146
Db 61 PTSSASKAYSALIEAIOKNATAFKGYAFKTYNTILGADDLTPFGEQOMVNSGKIFERY 120
Qy 147 YKALARKIVPPIRAGSDRVIASAEKIEGFSQAKLADPGANPHQASPVINVIPEGAGY 206
Db 121 YKALARKIVPPIRAGSDRVIASAEKIEGFSQAKLADPGANPHQASPVINVIPEGAGY 180
Qy 207 NNTLDHGLCTAFEDSELGDDVEANFTALFAPARLEADLPVTLTDEDVYVLMDCPF 240
Db 181 NNTLDHGLCTAFEDSELGDDVEANFTALFAPARLEADLPVTLTDEDVYVLMDCPF 240
Qy 267 DTVARTSDATLSLSPFCALFTDHEWROYDYLSLGKYYGAGNPLGPAQGVFNELIAR 326
Db 241 DTVARTSDATLSLSPFCALFTDHEWROYDYLSLGKYYGAGNPLGPAQGVFNELIAR 300
Qy 327 LTHSPVDHTSTNHTLDSNPATPLNATLYADFSHDNTMYSIFFALGLYNGTKPLSTTSV 386
Db 301 LTRSPVDHTSTNHTLDSNPATPLNATLYADFSHDNTMYSIFFALGLYNGTKPLSTTSV 360
Qy 387 ESIEETDGYASMTVPFAARAYVEMMOCEAREKPELVRVLVNDVRVPLHGCGVCKLGRCKR 446
Db 361 ESIEETDGYASMTVPFAARAYVEMMOCEAREKPELVRVLVNDVRVPLHGCGVCKLGRCKR 420
Qy 447 DDFVEGLSFARSGGNWEECEFA 467
Db 421 DDFVEGLSFARSGGNWEECEFA 441

RESULT 4
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:

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; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121.425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-121-425-2

Query Match      87.94; Score 2170; DB 3; Length 467;
Best Local Similarity 85.44; Pred. No. 2.2e-215;
Matches 416; Conservative 11; Mismatches 20; Indels 40; Gaps 2;

QY 1 MGVFVLLSLATLFGSTSGTALGPRGNSHSCDVTGGYQCFCPEISHLWGTYSPEFSLADE 60
DB 1 MGVFVLLSLATLFGSTSGTALGPRGNSHSCDVTGGYQCFCPEISHLWGTYSPEFSLEDE 60
QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFKLYN 120
DB 61 SAISPDVPDCCRVTFVQVLSRHGARYPTSSKAYSALIEAIOKNATAFKGYAFKLYN 100
QY 121 YTLGADDLTPGEOOMVNSGKIFRYRYKALARKIVPPIRASGSDRVIASAEKIEGFOSA 180
DB 101 YTLGADDLTPGEOOMVNSGKIFRYRYKALARKIVPPIRASGSDRVIASAEKIEGFOSA 160
QY 181 KLADPGANPHQASPVIN-----VIIPEGAGYNNTLDHGLCTAFEE 220
DB 161 KLADPGSQPHQASPVIDLIEAIOKNATAFKGYAFKLYNIIPEGAGYNNTLDHGLCTAFED 220
QY 221 SELGDDVEANTVAFPIRLEAHLPGVNLTDVVDVNMDCMCPDVTARTSDATQLSP 280
DB 221 SELGDDVEANTVAFPIRLEAHLPGVNLTDVVDVNMDCMCPDVTARTSDATQLSP 280
QY 281 FCDLTHDEWQYDYLQSLGKYGYGAGNPLGPAQGYGVFNELIARLTHSPVODHTSTNH 340
DB 281 FCALETHDEWQYDYLQSLGKYGYGAGNPLGPAQGYGVFNELIARLTHSPVODHTSTNH 340
QY 341 TLDSPATFPLNATLYADFSDHNTWVSIFFALGLYNGTKPLSTTSVESIEETGYSASWT 400
DB 341 TLDSPATFPLNATLYADFSDHNTWVSIFFALGLYNGTKPLSTTSVESIEETGYSASWT 400
QY 401 VPFAARAYVENMQCAEKEPLRVLVNDRVVPLHGCAGVDKLGRCRKRDDFVEGLSFARSGG 460
DB 401 VPFGARAYVENMQCAEKEPLRVLVNDRVVPLHGCAGVDKLGRCRKRDDFVEGLSFARSGG 460
QY 461 NWEECFA 467
DB 461 NNAECFA 467
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RESULT 5

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US-09-634-493A-2
; Sequence 2, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634.493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121.425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
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; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-634-493A-2
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Query Match 87.94; Score 2170; DB 4; Length 467;

Best Local Similarity 85.44; Pred. No. 2.2e-215;

Matches 416; Conservative 11; Mismatches 20; Indels 40; Gaps 2;

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QY 1 MGVFVLLSLATLFGSTSGTALGPRGNSHSCDVTGGYQCFCPEISHLWGTYSPEFSLADE 60
DB 1 MGVFVLLSLATLFGSTSGTALGPRGNSHSCDVTGGYQCFCPEISHLWGTYSPEFSLEDE 60
QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFKLYN 120
DB 61 SAISPDVPDCCRVTFVQVLSRHGARYPTSSKAYSALIEAIOKNATAFKGYAFKLYN 100
QY 121 YTLGADDLTPGEOOMVNSGKIFRYRYKALARKIVPPIRASGSDRVIASAEKIEGFOSA 180
DB 101 YTLGADDLTPGEOOMVNSGKIFRYRYKALARKIVPPIRASGSDRVIASAEKIEGFOSA 160
QY 181 KLADPGANPHQASPVIN-----VIIPEGAGYNNTLDHGLCTAFEE 220
DB 161 KLADPGSQPHQASPVIDLIEAIOKNATAFKGYAFKLYNIIPEGAGYNNTLDHGLCTAFED 220
QY 221 SELGDDVEANTVAFPIRLEAHLPGVNLTDVVDVNMDCMCPDVTARTSDATQLSP 280
DB 221 SELGDDVEANTVAFPIRLEAHLPGVNLTDVVDVNMDCMCPDVTARTSDATQLSP 280
QY 281 FCDLTHDEWQYDYLQSLGKYGYGAGNPLGPAQGYGVFNELIARLTHSPVODHTSTNH 340
DB 281 FCALETHDEWQYDYLQSLGKYGYGAGNPLGPAQGYGVFNELIARLTHSPVODHTSTNH 340
QY 341 TLDSPATFPLNATLYADFSDHNTWVSIFFALGLYNGTKPLSTTSVESIEETGYSASWT 400
DB 341 TLDSPATFPLNATLYADFSDHNTWVSIFFALGLYNGTKPLSTTSVESIEETGYSASWT 400
QY 401 VPFAARAYVENMQCAEKEPLRVLVNDRVVPLHGCAGVDKLGRCRKRDDFVEGLSFARSGG 460
DB 401 VPFGARAYVENMQCAEKEPLRVLVNDRVVPLHGCAGVDKLGRCRKRDDFVEGLSFARSGG 460
QY 461 NWEECFA 467
DB 461 NNAECFA 467
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RESULT 6

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US-08-858-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221
; GENERAL INFORMATION:
; APPLICANT: Van Loon, Adolphus
; APPLICANT: Mitchell, David
; TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/868.435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/744,231
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: Case Docket 9339
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 465 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 104
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 119
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 205
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 228
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 337
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 374
; OTHER INFORMATION: /note="potential N-glycosylation site"
;
; US-08-868-435-33
;
; Query Match 76.5%; Score 1888; DB 3; Length 465;
; Best Local Similarity 76.9%; Pred. No. 2.9e-186;
; Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;
;
QY 1 MGVFVLLSIATLFGSTGALPGRGNSHSDTVDDGGYQCFPEISHLWGTSPFFSLADE 60
DB 1 MYTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDTVDLGYQCSPATSHLWGQYSPFFSLDE 59
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QY 61 SAISDPVPGCRVTVQVLSLRHGARYPTSSASKAYSALIEATOKNATAFKGKYAFKLTYN 120
DB 60 LSVSSKLPRDCRITLVQVLSLRHGARYPTSSKSKYKLVLTALQANATDFKCKFAFLXTYN 119
;
QY 121 YTLGADDLTPFGEQKVNNGIKFYRYKALARKIVPFIASGSDRVIASAEKFIEGTQSA 180
DB 120 YTLGADDLTPFGEQKVNNGIKFYRYKALARKIVPFIASGSDRVIASAEKFIEGTQQA 179
;
QY 181 KLADPGANPHASPVNTVIIPGAGVNTLDHGLCTAFESPLGDDVFANFTAVFAPPIR 240
DB 180 KLADPGAT-NRAAPALSVIIPSEFTNLTLDHGVTCKFEASQLGDVEAANTALFAPDIR 238
;
QY 241 ARLEAHLPGVNLTDVDWNLMDMCPDVTVARTSDATQLSPFCDLTFHDEWIQYDYLQSLG 300
DB 239 ARAEKHLPGVTLTDEWVSLMDMCSFDTVARTSDASQLSPFCOLTFHNEWKYKYNLQSLG 298
;
QY 301 KYGYGAGNPLGPAQGVGFVNEILARLTHSPVQDHTSTNHLDSNPATFPLNATLYADFS 360
DB 299 KYGYGAGNPLGPAOGIGFTNELLARLTRSPVQDHTSTNLTSLVSNPATFPLNATMYVDFS 358
;
;
; 361 HDNTMVSIFPAGLYNGTKPLSTTSVESIEETDGYSSASWTVPFAARAYVEMMOCEAEKEP 420
; 359 HDNSMVSIFPAGLYNGTEPLSRTSVESAKELDGYSSASWVVPFGARAYFETMOCKSEKEP 418
;
; 421 LVRVLNDRVYPLHGGVCKLGRCKRDFVEGLSFABSGGNWEECEFA 467
; 419 LVRALINDRVYPLHGGCDVDKLGKGRCKLNDVFKGLSWARSGGNWGECEFS 465
;
;
; RESULTS 7
; US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
; GENERAL INFORMATION:
; APPLICANT: Van Loon, Adolphus
; APPLICANT: Mitchell, David
; TITLE OF INVENTION: POLYPRPTIDES WITH PHYTASE ACTIVITY
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/744,231
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/424,757
; FILING DATE: 18-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: Case Docket 9339
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 465 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 104
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 119
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 205
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 228
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 337
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 374
; OTHER INFORMATION: /note="potential N-glycosylation site"
;
; US-08-868-435-33

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LOCATION: 374
OTHER INFORMATION: /note="potential N-glycosylation site"
US-08-744-231-33

Query Match 76.5%: Score 1888; DB 4; Length 465;
Best Local Similarity 76.9%: Pred. No. 2.9e-186;
Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;

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QY 1 MGVEVLLSIATLFGSTGTALGPRGNSHSCDVTGGYQCQCFEISHLWGTSPPFSLADE 60
DB 1 MYTLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGQSPFFSLEDE 59
QY 61 SAISPDVPKGCRTVFOVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFLKTYN 120
DB LSVSSKLPKDCRITLVQVLSRHGARYPTSSASKYKLVTAIOANATDFKGFALKTYN 119
QY 121 YTLGADDLTPFGEQOMVNSGKIFYRRYKALARKIVPFIRASGSDRVIASAEKFIQFQSA 180
DB YTLGADDLTPFGEQOLVNSGKIFYQRYKALARSVVPFIRASGSDRVIASGEKFIQFQQA 179
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPDIR 240
DB KLADPGAT-NRAAPALSVIIESETFNNTLDHGVCCTKFEASQLGDEVAANFTALFAPDIR 238
QY 241 ARLEAHLPGVNLTDDEVDVSLMDKCFDVTARTSDATQISPCDLFTHDEWIQYDIQSLG 300
DB ARAEKHLPGVTLTDDEVDVSLMDKCFDVTARTSDASQISPCQLFTHNEWKYNYLQSLG 298
QY 301 KYCYGAGNPLGPAQGVGNELIARLTHSPVODHTSTNHTLDSNPATFFPLNATLYADES 360
DB KYCYGAGNPLGPAQGVGNELIARLTHSPVODHTSTNSTLYSNPATFFPLNATMYVDFS 358
QY 361 HDNTWYSIFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFARAYVEMMOCEAKEP 420
DB HDNSWVSIFFALGLYNGTEPLSRTSVESAKELDGYASWVYFGARAYFETMOCKSEKEP 418
QY 421 LVRYLVNDRVPLHGGVDKLGCRCKRDDFVEGLSFARSGGNWEECFA 467
DB LVRALINDRVPLHGGVDKLGCRCKLNDVFKGLSWARSGGNWEECFS 465
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RESULT 8

US-09-044-718-78
Sequence 78, Application US/09044718
Patent No. 6391605

GENERAL INFORMATION:
APPLICANT: KOSTREWA, Dirk
APPLICANT: PASAMONTES, Luis
APPLICANT: TOMSCHY, Andrea
APPLICANT: van LOON, Adolphus
APPLICANT: VOGEL, Kurt
APPLICANT: WESS, Markus
TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: Modified Phytases
CURRENT APPLICATION NUMBER: US/09/044,718
CURRENT FILING DATE: 1998-03-19
PRIOR FILING DATE: 1997-03-25
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 78
LENGTH: 465
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-09-044-718-78

Query Match 76.5%: Score 1888; DB 4; Length 465;
Best Local Similarity 76.9%: Pred. No. 2.9e-186;
Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;

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QY 1 MGVEVLLSIATLFGSTGTALGPRGNSHSCDVTGGYQCQCFEISHLWGTSPPFSLADE 60
DB 1 MYTLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGQSPFFSLEDE 59
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QY 61 SAISPDVPKGCRTVFOVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFLKTYN 120
DB LSVSSKLPKDCRITLVQVLSRHGARYPTSSASKYKLVTAIOANATDFKGFALKTYN 119
QY 121 YTLGADDLTPFGEQOMVNSGKIFYRRYKALARKIVPFIRASGSDRVIASAEKFIQFQSA 180
DB YTLGADDLTPFGEQOLVNSGKIFYQRYKALARSVVPFIRASGSDRVIASGEKFIQFQQA 179
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPDIR 240
DB KLADPGAT-NRAAPALSVIIESETFNNTLDHGVCCTKFEASQLGDEVAANFTALFAPDIR 238
QY 241 ARLEAHLPGVNLTDDEVDVSLMDKCFDVTARTSDATQISPCDLFTHDEWIQYDIQSLG 300
DB ARAEKHLPGVTLTDDEVDVSLMDKCFDVTARTSDASQISPCQLFTHNEWKYNYLQSLG 298
QY 301 KYCYGAGNPLGPAQGVGNELIARLTHSPVODHTSTNHTLDSNPATFFPLNATLYADES 360
DB KYCYGAGNPLGPAQGVGNELIARLTHSPVODHTSTNSTLYSNPATFFPLNATMYVDFS 358
QY 361 HDNTWYSIFFALGLYNGTKPLSTTSVESIEETDGYASWTVPFARAYVEMMOCEAKEP 420
DB HDNSWVSIFFALGLYNGTEPLSRTSVESAKELDGYASWVYFGARAYFETMOCKSEKEP 418
QY 421 LVRYLVNDRVPLHGGVDKLGCRCKRDDFVEGLSFARSGGNWEECFA 467
DB LVRALINDRVPLHGGVDKLGCRCKLNDVFKGLSWARSGGNWEECFS 465
```

RESULT 9

US-09-636-499-6
Sequence 6, Application US/09636499
Patent No. 6475762

GENERAL INFORMATION:
APPLICANT: Stafford, Christian F.
APPLICANT: Trinci, Anthony P.J.
APPLICANT: Brookman, Jayne L.

TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Sam
FILE REFERENCE: GC586-2
CURRENT APPLICATION NUMBER: US/09/636,499
CURRENT FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: US 60/148,960
PRIOR FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 465
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-09-636-499-6

Query Match 76.5%: Score 1888; DB 4; Length 465;
Best Local Similarity 76.9%: Pred. No. 2.9e-186;
Matches 359; Conservative 35; Mismatches 71; Indels 2; Gaps 2;

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QY 1 MGVEVLLSIATLFGSTGTALGPRGNSHSCDVTGGYQCQCFEISHLWGTSPPFSLADE 60
DB 1 MYTLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGQSPFFSLEDE 59
QY 61 SAISPDVPKGCRTVFOVLSRHGARYPTSSASKAYSALIEAIOKNATAFKGYAFLKTYN 120
DB LSVSSKLPKDCRITLVQVLSRHGARYPTSSASKYKLVTAIOANATDFKGFALKTYN 119
QY 121 YTLGADDLTPFGEQOMVNSGKIFYRRYKALARKIVPFIRASGSDRVIASAEKFIQFQSA 180
DB YTLGADDLTPFGEQOLVNSGKIFYQRYKALARSVVPFIRASGSDRVIASGEKFIQFQQA 179
QY 181 KLADPGANPHQASPVINVIIEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAPDIR 240
DB KLADPGAT-NRAAPALSVIIESETFNNTLDHGVCCTKFEASQLGDEVAANFTALFAPDIR 238
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RESULT 12

US-09-044-718-79
: Sequence 79, Application US/09044718
: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: Modified Phytases
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: NUMBER OF SEQ ID NOS: 25
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 79
: LENGTH: 465
: TYPE: PRI
: ORGANISM: Aspergillus fumigatus
US-09-044-718-79

Query Match 76.1% Score 1879; DB 4; Length 465;

Best Local Similarity 76.7% Pred. No. 2.5e-185;
Matches 350; Conservative 35; Mismatches 72; Indels 2; Gaps 2;

QY	1	MGVFWLLSIATLFGSTGALGPRNSHSCDVTGQYQCFPEISHLWGTSPFFSLADE	60
DB	1	MVLTLLSAAYLLSGRVSAAPSSAG-SKSCDIVDVGQSPATSHLWQYSPFFSLADE	59
QY	61	SATSPDVPKCRVTFVQVLSRHGARYPTSSAKAYSALIEAQKNATAKGYAFKLTYN	120
DB	60	LSVSSKLPKDCRITLVQVLSRHGARYPTSSKKYKLVTAIQANATDFKGFALFKTYN	119
QY	121	YTLGADDLTPFGQQQVMNSGKFKYRYKALKARKIVPFIASGSDRVIASAEKFIQFQA	180
DB	120	YTLGADDLTPFGQQQVMNSGKFKYRYKALKARSVPFIASGSDRVIASAEKFIQFQA	179
QY	181	KLADPGANPHQASPVINVIPEGAGYNNITLDHGLCTAFEESELGDDVEANFTAVFAP	240
DB	180	KLADPGAT-NRAAPATSVIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDR	238
QY	241	ARLEAHLPGVNLTDDEVVNLMDMCPDVTVAKTSDATQLSPFCGLFTHDEWIQYDYLQSLG	300
DB	239	AREKHLPGVNLTDDEVVNLMDMCSFTVARTSDASQLSPFCGLFTHDEWIQYDYLQSLG	298
QY	301	KYGYGAGNPLGPAQGVGFVNNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYAFDS	360
DB	299	KYGYGAGNPLGPAQGGIGFTNELIARLTHSPVQDHTSTNHTLDSNPATFPLNATMIVDFS	358
QY	361	HDNTWVSIFPAGLYNCKLPSTTSVESIEETDGYASATVPPFAARAYVENMOCEAEKEP	420
DB	359	HDNSWVSIFPAGLYNCKLPSTTSVESIEETDGYASATVPPFAARAYVENMOCEAEKEP	418
QY	421	LVRVLVNDRVVPLHGGGVNDKLGCRKDDFVEGLSFARSGGNWCECFA 467	
DB	419	LVRALINDRVVPLHGGGVNDKLGCRKLNDFVKGLSWARSGGNWCECFS 465	

RESULT 13

US-09-044-718-3
: Sequence 3, Application US/09044718
: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus

: TITLE OF INVENTION: Modified Phytases
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3
: LENGTH: 439
: TYPE: PRI
: ORGANISM: Aspergillus fumigatus
US-09-044-718-3

Query Match 76.1% Score 1878.5; DB 4; Length 439;

Best Local Similarity 79.8% Pred. No. 2.6e-185;
Matches 351; Conservative 35; Mismatches 53; Indels 1; Gaps 1;

QY	28	SHSCDVTGQYQCFPEISHLWGTSPFFSLADESAISPDVPKCRVTFVQVLSRHGARYP	87
DB	1	SKSCDVTGQYQCFPEISHLWGTSPFFSLADELSVSKLPKCKRITLVQVLSRHGARYP	60
QY	88	TSSAKAYSALIEAQKNATAKGYAFKLTYNITLGDADLTPEGEQQVMNSGKFKYRY	147
DB	61	TSSSKYKLVTAIQANATDFKGFALFKTYNTLGDADLTPEGEQQVMNSGKFKYRY	120
QY	148	KALARKIVPFIASGSDRVIASAEKFIQFQSAKLADPGANPHQASPVINVIPEGAGYN	207
DB	121	KALARSVPFIASGSDRVIASAEKFIQFQSAKLADPGAT-NRAAPATSVIPESETFN	179
QY	208	NTHDGLCTAFEESELGDDVEANFTAVFAPPIARLEAHLPGVNLTDDEVVNLMDMCPD	267
DB	180	NTHDGLCTAFEESELGDDVEANFTALFAPDIRAKELHPLGVTLTDDEVVNLMDMCSFD	239
QY	268	TVARTSDAQLSPFCGLFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGVGFVNNELIARL	327
DB	240	TVARTSDASQLSPFCGLFTHDEWIQYDYLQSLGKYGYGAGNPLGPAQGGIGFTNELIARL	299
QY	328	THSPVQDHTSTNHTLDSNPATFPLNATLYAFDSHDNTWVSIFPAGLYNCKLPSTTSVE	387
DB	300	TRSPVQDHTSTNHTLDSNPATFPLNATMIVDFSHDNSWVSIFPAGLYNCKLPSTTSVE	359
QY	388	SIETDGYASATVPPFAARAYVENMOCEAEKEPDLVRVLVNDRVVPLHGGGVNDKLGCRK	447
DB	360	SAKELDGYASATVPPFAARAYVENMOCEAEKEPDLVRALINDRVVPLHGGGVNDKLGCRKLN	419
QY	448	DFVEGLSFARSGGNWCECFA 467	
DB	420	DFVKGLSWARSGGNWCECFS 439	

RESULT 14

US-09-044-718-12
: Sequence 12, Application US/09044718
: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: Modified Phytases
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 12
: LENGTH: 449
: TYPE: PRI

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: ORGANISM: Aspergillus fumigatus
US-09-044-718-12

Query Match          76.1%; Score 1878.5; DB 4; Length 449;
Best Local Similarity 79.8%; Pred. No. 2.6e-185;
Matches 351; Conservative 35; Mismatches 53; Indels 1; Gaps 2;

Qy 28 SSSCTVDGCGYCFEISHLWGTYSPPFSLADESAISPDVPGKGRVTVQVLSRHGARYP 87
Db 11 SKSCDVTDLGYCSPATSHLWQYSPFFSLEDELVSVKLPKCRITLTVQVLSRHGARYP 70

Qy 88 TSSASKAYSALTEAKNATAPKGYAFUKTYNYTLGADDLTPGCEQMVNSGKFYRRY 147
Db 71 TSSKSKYKKLWTAQANATDFKFAFLKTYNYTLGADDLTPGCEQMVNSGKFYRRY 130

Qy 148 KALARKIVPFIKASGSDRVIAAEKPIEGFQSAKIALDPGANPHOASPVNVIPEGAGYN 207
Db 131 KALARSVWPFIRASGSDRVIAAEKPIEGFQSAKIALDPGANPHOASPVNVIPEGAGYN 189

Qy 208 NTLDHGLCTAFEESELGDDVEANFTAVFAPTRARLEAHLPGVNLTDSDVNLMDMCPD 267
Db 190 NTLDHGVCYTKFASQGLGDEVAANFTALFAPDIRARAEKHLPGVNLTDSDVNLMDMCPD 249

Qy 268 TVARTSDATQSPFCDFTHDWMQYDYLSLQSLGKYGYGAGNPLGPAQGVGVNLIARL 327
Db 250 TVARTSDATQSPFCDFTHDWMQYDYLSLQSLGKYGYGAGNPLGPAQGVGVNLIARL 309

Qy 328 THSPVDHTSTNHTLDSNPATPLNATLYADFSHONTWYSIFFALGLYNGTKPISTSYE 387
Db 310 THSPVDHTSTNHTLDSNPATPLNATLYADFSHONTWYSIFFALGLYNGTKPISTSYE 369

Qy 388 SIBEDIGYASMTVPFAARAYVEMMOCEAEKEPLVRLVNDRVVPLHGGCVDKLGRCKRD 447
Db 370 SAKELDGYASWVVPFGARAYFETMOCKSEKEPLVRLVNDRVVPLHGGCVDKLGRCKLN 429

Qy 448 DFVEGLSFARSGGNWEECEFA 467
Db 430 DFVKGLSWARSGGNWGECEFS 449
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```

RESULT 15
US-09-044-718-81
: Sequence 81. Application US/09044718
: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WISS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: CURRENT FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: Patent In Ver. 2.1
: SEQ ID NO 81
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-09-044-718-81
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Query Match          76.0%; Score 1876; DB 4; Length 465;
Best Local Similarity 76.4%; Pred. No. 5.1e-185;
Matches 357; Conservative 36; Mismatches 72; Indels 2; Gaps 2;

Qy 1 MGVEFWLLSTATLFGSTSGTALPGRNHSHCDTVDCGYQCFEISHLWGTYSPPFSLADE 60
Db 1 MVTLTFLLSAAYLDSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWQYSPFFSLEDE 59
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Title: US-09-488-265B-30

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	2308	92.5	457	14	US-10-083-452-9	Sequence 9, Appl.
2	1888	75.9	465	14	US-10-083-452-8	Sequence 8, Appl.
3	1888	75.9	465	15	US-10-062-848-78	Sequence 78, Appl.
4	1888	75.9	465	15	US-10-229-358-6	Sequence 6, Appl.
5	1881.5	75.7	474	15	US-10-213-990-24	Sequence 24, Appl.
6	1880	75.6	465	15	US-10-062-848-80	Sequence 80, Appl.
7	1879	75.6	465	15	US-10-062-848-79	Sequence 79, Appl.
8	1878.5	75.6	439	15	US-10-062-848-3	Sequence 3, Appl.
9	1878.5	75.6	449	15	US-10-062-848-12	Sequence 12, Appl.
10	1876	75.5	465	15	US-10-062-848-81	Sequence 81, Appl.
11	1854	74.6	469	15	US-10-062-848-82	Sequence 82, Appl.
12	1848	74.3	467	15	US-10-079-709-32	Sequence 32, Appl.
13	1848	74.3	467	15	US-10-229-358-5	Sequence 5, Appl.
14	1841	74.1	467	9	US-09-929-060-3	Sequence 3, Appl.
15	1836	73.9	467	14	US-10-083-452-11	Sequence 11, Appl.
16	1829	73.6	462	15	US-10-229-358-12	Sequence 12, Appl.
17	1806	72.6	444	15	US-10-062-848-1	Sequence 1, Appl.
18	1804.5	72.6	463	14	US-10-083-452-20	Sequence 20, Appl.
19	1799	72.4	443	9	US-09-929-060-1	Sequence 1, Appl.
20	1794	72.0	443	9	US-09-929-060-2	Sequence 2, Appl.
21	1789.5	72.0	447	15	US-10-062-848-6	Sequence 6, Appl.
22	1752	70.5	466	14	US-10-083-452-12	Sequence 12, Appl.
23	1752	70.5	466	15	US-10-229-358-7	Sequence 7, Appl.
24	1748	70.3	450	15	US-10-062-848-15	Sequence 15, Appl.
25	1710	68.8	466	14	US-10-083-452-13	Sequence 13, Appl.
26	1706.5	68.6	450	15	US-10-062-848-9	Sequence 9, Appl.
27	1697	68.3	438	15	US-10-062-848-2	Sequence 2, Appl.
28	1658	66.7	489	15	US-10-229-358-4	Sequence 4, Appl.
29	1658	66.7	489	15	US-10-229-358-10	Sequence 10, Appl.
30	1623	65.3	410	15	US-10-229-358-11	Sequence 11, Appl.
31	1381	55.6	475	14	US-10-083-452-14	Sequence 14, Appl.
32	1339	53.9	355	15	US-10-229-358-15	Sequence 15, Appl.
33	1334.5	53.7	487	14	US-10-083-452-15	Sequence 15, Appl.
34	1334.5	53.7	487	15	US-10-229-358-8	Sequence 8, Appl.
35	1215	48.9	495	14	US-10-083-452-2	Sequence 2, Appl.
36	1210	48.7	478	14	US-10-083-452-3	Sequence 3, Appl.
37	920	37.0	284	15	US-10-229-358-19	Sequence 19, Appl.
38	867	34.9	283	15	US-10-229-358-9	Sequence 9, Appl.
39	867	34.9	283	15	US-10-229-358-24	Sequence 24, Appl.
40	845.5	34.0	443	14	US-10-083-452-5	Sequence 5, Appl.
41	833.5	33.5	453	14	US-10-083-452-6	Sequence 6, Appl.
42	830.5	33.4	439	14	US-10-083-452-7	Sequence 7, Appl.
43	825	33.2	442	14	US-10-083-452-4	Sequence 4, Appl.
44	729.5	29.3	212	15	US-10-229-358-16	Sequence 16, Appl.
45	406	16.3	312	15	US-10-229-358-21	Sequence 21, Appl.

ALIGNMENTS

RESULT 1

US-10-083-452-9
; Sequence 9, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Ailan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083.452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273.871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25

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; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
;
US-10-083-452-9

Alignment Scores:
Pred. No.:      2,79e-181      Length:      467
Score:          2308.00      Matches:      436
Percent Similarity: 95.72%      Conservative: 11
Best Local Similarity: 93.36%      Mismatches:   20
Query Match:      92.84%      Indels:       0
DB:              14          Gaps:          0

US-09-488-265B-30 (1-1404) x US-10-083-452-9 (1-467)

QY   1  ATGGCGCTGTCGTCGTCTACTGTCATTGCCACCTTGTTCGGTTCACATCCGGTACC 60
Db   1  MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20
QY   61  GCCTTGGCTCTCGTGGTAACTCTACCTCTGTGCACACICTTCACCGTGGTACCAAGT 120
Db   21  AlaLeuGlyProAAGLYAsnSerHisSerCysAspThrValAspGlyGlyIyrGlnCys 40
QY   121  TTCCGAGAAATTTCTCACTTGTGGGGTACATCTCTCCATCTCTCTTTCGGTGCACGA 180
Db   41  PheProGluIleSerHisLeuTrpGlyClnIyrSerProTyrPheSerLeuGluAspGlu 60
QY   181  TCTGCTATTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTTCGT 240
Db   61  SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80
QY   241  AGACAGGCTGTAGATACCCAACTCTTCTCGCTTAAGCGGTACTCTGCTTTGATGAA 300
Db   81  ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGlu 100
QY   301  GCTATTCAAAGAACGCTACTGCTTCAAGGCTAAAGTACGCTTCTTGAAGACTTCAAC 360
Db   101  AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAs 120
QY   361  TACACTTTGGTGTCTGACGACTTGACTCCATTCGCTGCAACAACAATGGTAACTCTG 420
Db   121  TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 140
QY   421  ATTAACCTTCTACASAAGATACAAAGCCTTGGCTACAAAGATTCTTCCATTTCATTAG 480
Db   141  IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 160
QY   481  TCTGGTCTGCAGAGACTTATTCGCTCTGCTGCAAAAGTTCATTGAAGGTTCCGAACT 540
Db   161  SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 180
QY   541  AAGTTGGCTGACCCAGGTGCTAAACCCACCAAGCTCTTCCCASTATTATTAAGTTATT 600
Db   181  LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspValIleIle 200
QY   601  CCAGAGGTCGTGTTTACAACAACACTTTGACCAACCGTTCGTACTGCTGCTTCGAGAA 660
Db   201  ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220
QY   661  TCTGAATGGGTGACGACGTTGAAGCTAACTCACTGCTGCTTTTCGCTCCCACTTAGA 720
Db   221  SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
QY   721  GCTAGATTGGAAGCTCACTTCCAGGCTGTTAACTTGACTGACGACGAGCTGTGTACT 780
Db   241  AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 840
QY   781  ATGGACATGTGTCATTGACACTGTTCCTAGAACTTCTGACGCTACTCAATTGCTCCCA 840

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US-10-083-452-8

Alignment Scores:	
Pred. No.:	9,978-247
Score:	1888.00
Percent Similarity:	84.37%
Best Local Similarity:	76.87%
Query Match:	75.95%
DB:	14
	2
Length:	465
Matches:	359
Conservative:	35
Mismatches:	71
Indels:	2
Gaps:	2

US-09-488-265B-30 (1-1404) X US-10-083-452-8 (1-465)

QY	1	ATGGCGGTGCTGCTGCTACTGCTCATTTGCCACCTGTGTTCGGTTCACACATCCGGIACC	60
DB	1	MetValThrLeuThrPheLeuLeuSerAlaAlaThrLeuLeuSerGlyArgValSerAla	20
QY	61	GCGTTGGGTCCGTGGTGAATCTCACTCTGTGCACACTGTTGCACGGTGGTACCAATG	120
DB	21	AlaProSerSerAlaGly--SerLysSerCysAspThrValAspLeuGlyThrGlnCys	39
QY	121	TTCCAGAAATTTCTCACTTGTGGGTACATCTCTCCATCTCTCTTTGGCTGACGAA	180
DB	40	SerProAlaThrSerHisLeuTrpGlyClnThrSerProPheSerLeuGlnAspGlu	59
QY	181	TCTGTATTCTCCAGAGTTCCAAAGGGTTGATAGCTTACTTCTGTTCAAGTTTGTCT	240
DB	60	LeuSerValSerSerLysLeuProGlyAspCysArgIleThrLeuValGlnValLeuSer	79
QY	241	AGACACGGTGTGATACCCAACTCTCTCTGCGTCTAAGCGGTACTCTGCTTTGATGAA	300
DB	80	ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLysLeuValThr	99
QY	301	GCTATTCAAAGAACGCTACTGCTTCAAGGGTAAG-ACGCTTCTTGAGACTTACAC	360
DB	100	AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn	119
QY	361	TACATTTGGGTGTGACGACTTGACTCCATTCGGTGAACACAAATGGTTAACTCTGT	420
DB	120	TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGlnGlnLeuValAsnSerGly	139
QY	421	ATTAAAGTTCTACAGAGATACAAAGCCTTGGCTAGAAGATTGTTCCATTCATTAGAGT	480
DB	140	IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla	159
QY	481	TCTGGTCTGCACAGAGTTATTGCTTCTGCTGAAAGTTTCATTGAAGGTTTCCAACTGCT	540
DB	160	SerGlySerAspArgValIleAlaSerGlyGlyLysPheIleGlyGlyPheGlnAla	179
QY	541	AGTTGGCTGACCCAGGTGCTTAACCCACACCAAGCTTCTCCAGTTATTACGTTATTAIT	600
DB	180	LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle	198
QY	601	CCAGAAGTGCTGTTACAAACACACTTGCACACCGGTTGTGACTGCTTTCGAAGA	660
DB	199	ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla	218
QY	661	TCTGAATTTGGGTGACAGCGTTCAAGCTTAACCTGCTGTTTTCGGTCCACCAATTAGA	720
DB	219	SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg	238
QY	721	GCTAGATTGGAAGCTCACTTGCACGGTCTTAACTTGAATGACGAAGCGTTGTTAACTGT	780
DB	239	AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu	258
QY	781	ATGACATGTTGCCATTGCACACTGTTGCTAGAACTTCTTGACGCTACTCAATTTGTTCCA	840
DB	259	MetAspMetCysSerPheAspThrValAlaAlaArgThrSerAspAlaSerGlnLeuSerPro	278
QY	841	TCTGTGACTTGTCTCACTCACACCAATGGATTCAATACGACTACTTGCATCTTTGGGT	900
DB	279	PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly	298
QY	901	AAGTACTACGGTTACGGTGCIGCTGAACCCATTGGGTCCAGCTCAAGGTGTGCTTTCGTT	960

Db	299	LysTyrTyrGlyTyrGlyValGlyAsnProLeuGlyProAlaGlnGlyLeuGlyPheThr	318
Qy	961	AACGAATTGATTGGTAGATTGACTCCTCCAGITTCACAGACACACTCTACTAACCCAC	1020
Lb	319	AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer	336
Qy	1021	ACTTTGGACTCTAACCCAGTACTTTCCTCCATTGAACGCTACTTTCTAGCGTGACTTCTCT	1080
Db	339	ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetCysValAspPheSer	358
Qy	1081	CACGACAACTATGGTTTCTATTTCCTTCGGTTTGGGTTTGTACACGGTACTAAGCCA	1140
Db	359	HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro	378
Qy	1141	TGTCTACTACTCTGTGGAACTATTGAAGAACCTACGGTTACTCTGCTTCTTGACT	1200
Db	379	LeuSerArgThrSerValGluSerAlaLeuLysGluLeuAspGlyTyrSerAlaSerIrpVal	398
Qy	1201	GTTCCATTGCGTGTAGACGTTAGCTTGAATGATGCAATGTGAAGCTGAAAGGAACCA	1260
Db	399	ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro	418
Qy	1261	TGTGGTTAGAGTTTGGTTTAAACGACAGAGTTGTTCCATTGCACGGTGTGGTGTCACAAAG	1320
Db	419	LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys	438
Qy	1321	TTGGGTAGATGTACAGACAGACGACTTCGTTTCAGAGTTTGTCTTTGCTAGATCTGGTGGT	1380
Db	439	LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerIrpAlaArgSerGlyGly	458
Qy	1381	AACTGGGAGAGATGTTTCGT	1401
Db	459	AsnIrpGlyGluCysPheSer	465

RESULT 3

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US-10-062-948-78
: Sequence 78, Application US/10062848
: Publication No. US20030092155A1
: GENERAL INFORMATION:
: APPLICANT: KOSTRENA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn ver. 2.1
: SEQ ID NO 78
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
: US-10-062-848-78

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Alignment Scores:		
Pred. No.:	9,97e-147	Length:
Score:	1888.00	Matches:
Percent Similarity:	84.37%	Conservative:
Rest local Similarity:	76.87%	Mismatches:
Query Match:	75.95%	Indels:
DB:	15	Gaps:
	2	
		465

US-09-488-265B-30 (1-1404) X US-10-062-848-78 (1-465)

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Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
Qy 61 GCCTGGTGGTCTCGTGAACCTCTACTCTGTGACACTGTGTGACGGTGGTATACCAAGT 120
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
Qy 121 TTCCAGAAATTTCTCACTGTGGGGGTACATCTCCATCTTCTCTTTGGCTGACGAA 180
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
Qy 181 TCTGCTATTCTCCACAGCTTCCAAAGGCTCTACAGTTACTTTCTGTTCAAGTTTGTCT 240
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
Qy 241 AGACAGGCTGTAGATACCCAACTTCTTCTGCGCTAAAGGCTACTCTGCTTTGATTGAA 300
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLeuValThr 99
Qy 301 GCTATTCAAAGACGCTACTGCTTTCAGGGTAAAGTACGCTTTCTTGAAGCTTACCAAC 360
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
Qy 361 TACACTTTGGGTCTGACGACTTGATCCATTCGGTGAACAAATGCTTAACCTCTGCT 420
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
Qy 421 ATTAAGTTCTACAGAGATACAGGCTTTGGCTAGAAAGATTGTTCCATTCAATAGCT 480
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
Qy 481 TCTGGTCTGACAGAGTATTGCTTCTGCTGAAAGTTCAITGAAGTTTCCAACTCTGCT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
Qy 541 AAGTTGGCTGACCCAGCTGCTTAACCCACACAGCTTCTCCAGTTATTAACTATTATT 600
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
Qy 601 CCAGAAGTCTGTTTACACACACTTTGGACCGGTTTGTGATGCTGCTTCCAAAGAA 660
Db 199 ProGlnSerGlnThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 216
Qy 661 TCTGAATTTGGCTGACGAGCTTGAAGCTTAACCTACACGCTGTTTCCGCTCCACAAITAGA 720
Db 219 SerGlnLeuGlyAspGluAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
Qy 721 GCTAGATTGGAAGCTCACTTCCAGAGTGTAACTTGACTGACGAAGAGCTGTGTAACCTG 780
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
Qy 781 ATGGACATGTGTCATTCGACACTGTGTGCTAGAACTTCTGACGCTACTCAATTTGCTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaAlaArgThrSerAspAlaSerGlnLeuSerPro 278
Qy 841 TCTGCTGACTTGTCTACITCAGCAGGAATGGATTCATACGACTACTTCCAACTTTGGGT 900
Db 279 PheCysGlnLeuPheThrHisAsnGlnTyrLysLysTyrAsnTyrLeuGlnSerLeuGly 298
Qy 901 AAGTACTACGGTTACGGTGTGCTAAACCCATTTGGGTCCAGCTCAAGGTTGTTGTTTCT 960
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
Qy 961 AACGAATTGATTGCTAGATTGACTACTCTCCAGTTTCAAGACACACTTCTACTTAACAC 1020
Db 319 AsnGlnLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
Qy 1021 ACTTGTGACTCTAACCCAGCTACTTTCCTCATTTGAACGCTACTTTGTACGCTGACTTCT 1080
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
Qy 1081 CAGCACAACTATGTTTCTATTCTTCTGCTTTGGGTTTGTACAACGCTACTAAGCA 1140
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Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
Qy 1141 TGTCTACTACTTCTTGAATCTATGAAGAACTGACGGTACTCTCTCTCTTCTTGGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
Qy 1201 GTTCCATTGCTGCTAGAGCTTACGTTGAATGATGCAATGTGAAGCTGAAAGGACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
Qy 1261 TTGCTTAGAGTTTGTGTTAAACGACAGAGTTGTTCACTTGCACGGTGTGGTTCACAAG 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
Qy 1321 TTGGGTAGATGTAAGAGAGACGACTTCGTTGAAGTTTGTCTTTCGCTAGATCTGGTGT 1380
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
Qy 1381 AACTGGGAAGAATGTTTCGCT 1401
Db 459 AsnTrpGlyGluCysPheSer 465

RESULT 4
US-10-229-358-6
; Sequence 6, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trincl, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229.358
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148.960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-229-358-6

Alignment Scores:
Pred. No.: 9,97e-147 Length: 465
Score: 1888.00 Matches: 359
Percent Similarity: 84.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
DB: 15 Gaps: 2

US-09-488-265b-30 (1-1404) x US-10-229-358-6 (1-465)
Qy 1 ATGGGGGTGTTCGCTGCTACTGTCCATTCGACCTTGTTCGGTTCACATCCGCTACC 60
Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
Qy 61 GCCTTGGGTCTCGTGAACCTCTACTCTGTGACACTGTGTGACGGTGGTATACCAAGT 120
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
Qy 121 TTCCAGAAATTTCTCACTGTGGGGGTACATCTCCATCTTCTCTTTGGCTGACGAA 180
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
Qy 181 TCTGCTATTCTCCACAGCTTCCAAAGGCTCTACAGTTACTTTCTGTTCAAGTTTGTCT 240
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
Qy 241 AGACAGGCTGTAGATACCCAACTTCTTCTGCGCTAAAGGCTACTCTGCTTTGATTGAA 300
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Db      80 A-gHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLeuValThr 99
QY      301 GCTATTCAAAGAGCGCTACTCGTTCCTCAAGGTAAGTACGCTTCCTTGAAGACTACAAAC 360
Db      100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY      361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGCTGAACACAAATGGTTAACTCTGGT 420
Db      120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnLeuValAsnSerGly 139
QY      421 ATTAAGTTCTACAGAGATACAGGCTTGGCTAGAAAGATTGTTCCATTTCATAGAGCT 480
Db      140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValProPheIleArgAla 159
QY      481 TCTGGTCTTGACAGAGATTATTGCTCTGCTGAAAAGTTCATTGAAGGTTTCCAAATCTGCT 540
Db      160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
QY      541 AAGTTGGCTGACCGAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAAAGTATTAT 600
Db      180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
QY      601 CCAGAAGGTGCTGTTACAAACACACTTTGGACACGCTTTCGTACTGCTTTCGAAGAA 660
Db      199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 216
QY      661 TGTGAATTGGTGACGACGCTTGAAGCTTAAGCTTAAGTCTGCTGCTGCTCCACCAATAGA 720
Db      219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY      721 GCTAGATTGAGCACTCACCTGCGAGGTGTTAACTTGACTGACGACGAGAGCTGTTAACTTG 780
Db      239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY      781 ATGCATGATGTCCATTGACACACTGTGCTAGAACCTCTGACGCTACTCAATGTCTCCA 840
Db      259 MetAspMetCysSerPheAspThrValAlaAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY      841 TTTCTGACTGTTTCTACTCAGCAGCAATGATTCATACGACTACTTGCATCTTGGGT 900
Db      279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnIleLeuGlnSerLeuGly 298
QY      901 AAGTACTACGTTACGGTGTGTGTAACCATTTGGTCCAGCTCAAGGTGTTGGTTCGTT 960
Db      299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY      961 AAGCAATTGATTCCTAGATTGACTACTCTCCAGTTCAAGACACACACTCTACTAACCAAC 1020
Db      319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY      1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTCGACGCTACTTTGACGCTGACTCTCT 1080
Db      339 ThrLeuValSerAsnProAlaThrPheProLeuLysAlaThrMetTyrValAspPheSer 358
QY      1081 CAGCACAACTATGTTTCTATTTCCTGCTTTGGGTTTGTACACGGTACTAAGCCA 1140
Db      359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
QY      1141 TTGCTACTACTTCTGTTGAATCTATTGAAGAACTGACGGTACTCTGCTCTCTGGACT 1200
Db      379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
QY      1201 GTTCCATCTCCTGCTAGAGCTTACGTTGAATGATGCAATGTGAAGCTGAAAAGGAACCA 1260
Db      399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
QY      1261 TTGGTTAGAGTTTGGTTAACGACAGAGTTGTTCCATTTCACGGTGTGGTGTGACAGAC 1320
Db      419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY      1321 TTGGGTAGATCTAGACAGACGACTCTGTTGAAGGTTTGTCTTTCCTAGATCTGGTGT 1380
Db      439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
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QY      1381 AACTGGGAAGAATGTTTCGCT 1401
Db      459 AsnTrpGlyGluCysPheSer 465

RESULT 5
US-10-213-990-24
: Sequence 24, Application US/10213950
: Publication No. US20030082595A1
: GENERAL INFORMATION:
: APPLICANT: Jiang, Bo
: APPLICANT: Bussey, Howard
: APPLICANT: Storms, Reg
: APPLICANT: Roemer, Terry
: TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
: TITLE OF INVENTION: ENZYMES AND METHODS OF USE
: FILE REFERENCE: 10182-019-999
: CURRENT APPLICATION NUMBER: US/10/213,990
: CURRENT FILING DATE: 2002-08-05
: NUMBER OF SEQ ID NOS: 72
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 24
: LENGTH: 474
: TYPE: PRT
: ORGANISM: Aspergillus
US-10-213-990-24

Alignment Scores:
Pred. No.:      3,44e-146      Length:      474
Score:          1881.50      Matches:    355
Percent Similarity: 84.76%      Conservative: 40
Best Local Similarity: 76.18%      Mismatches: 64
Query Match:      75.68%      Indels:      7
Db:              15          Gaps:          2

US-09-488-265B-30 (1-1404) x US-10-213-990-24 (1-474)
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QY      4 GGGGTGTTCTCGTGTACTGCTCCATTGGCCACCTGTTGCGTTCACATCCGGTACCGGCC 63
Db      16 GlyAlaValValleuIleuLysArgSerArgValSerAlaAlaProSerSer----- 33
QY      64 TTGGGTCTCGTGGTAACCTCTCTGTGACACTGTTGACGGTGTTCACCAATGTTTC 123
Db      34 -----AlaGlySerLysSerCysAspThrValAspLeuGlyTyrGlnCysSer 49
QY      124 CCAGAAATTTCTCACTTGGGGTACATCTCCATTCTCTCTTGGCTGACCAATCT 183
Db      50 ProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeu 69
QY      184 GCTATTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCTAGA 243
Db      70 SerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSerArg 89
QY      244 CAGGTGCTAGATACCAACTTCTTTCGCTCTAAGCGTACTCTGCTTGATTGATTAAGCT 303
Db      90 HisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThrAla 109
QY      304 ATTCAAAAGAACGCTACTGCTTTCAGGGTAACTAGCTTCTTGAAGACTTACAACTAC 363
Db      110 IleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyr 129
QY      364 ACTTTGGGTGCTGACGACTTGACTTCCATTCGTTGGAACAAATGTTTAACTCTGTTAT 423
Db      130 ThrLeuGlyAlaAspLeuThrProPheGlyGluGlnLeuValAsnSerGlyIle 149
QY      424 AAGTCTACAGAACATACAAAGGTTGGCTAGAACAAATGTTCCATTTCATAGAGCTTCT 483
Db      150 LysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAlaSer 169
QY      484 GGTTCACAGAGTATTGCTTCTGCTGAAAAGCTTCATTGAAGGTTTCCAATCTGCTAAG 543
Db      170 GlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLys 189
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QY 544 TTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTATTAATCCCA 603
Db 190 LeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIlePro 208
QY 604 GAAGGTGCTGGTTACACAACTTTGGACCAAGGTTTGTACTGCTTTTCGAAGAICT 663
Db 209 GluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAlaSer 228
QY 664 GAATTGGGTGACACGCTTGAAGCTAACTCACTGCTGCTGTTTTCGCTCCACCAATTAGAGCT 723
Db 229 GluLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAla 248
QY 724 AGATTGGAAGCTCACTTCCAGGTTTAACTTGACGACGAAGCGTTGTGTAACTTGATG 783
Db 249 ArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeuMet 268
QY 784 GACATGTGCCATTGACACTGCTCTAGAACTTCTGACGCTACTCAATTCCTCCATTC 843
Db 269 AspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerProPhe 288
QY 844 TGTGACTTGTCTCACTCACGACGAATGATTCATACGACTACTTGCATCTTTGGGTAAAG 903
Db 289 CysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLys 308
QY 904 TACTAGGTTACGGTCTGCTGCTTACCCATTGGGTCCAGCTCAAGTGTGGTTTCGTTAAC 963
Db 309 TyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsn 328
QY 964 GAATTGATTCCTAGATTGACTCACTCTCCAGTTCAGACCACTTCTACTCAACACACACT 1023
Db 329 GluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSerThr 348
QY 1024 TTGACTCTAACCCACTACTTCCCATGCAAGCTACTTTGTAGCTGACTTCTCTCAC 1083
Db 349 LeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSerHis 368
QY 1084 GACAACACTATGTTTCTATTCTTCGCTTTGGTTTGTACAAAGGTACTAAAGCCATTG 1143
Db 369 AspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeu 388
QY 1144 TCTACTACTTCTGTTCAATCTATTGAGAACTGACCGTTACTCTGCTTCTTGGACTGTT 1203
Db 389 SerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValVal 408
QY 1204 CCATTGCTCTAGACCTTACGTTGAATGATGCAATGATGAAGCTGAAGAAAGAACCATIG 1263
Db 409 PropheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluProLeu 428
QY 1264 GTTAGACTTTTGGTTAACGACAGAGTCTTCCATTGCCAGGTTGTGGTTGTACAGAGTTG 1323
Db 429 ValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLysLeu 448
QY 1324 GGTAGATGTAAGAGACGACTTCTGTTGAAGTTTGTCTTTTCGCTAGATCTGGTGGTAAC 1383
Db 449 GlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyCysAsn 468
QY 1384 TGGGAAGATGTTTCGCT 1401
Db 469 TrpGlyGluCysPheSer 474
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RESULT 6

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US-10-062-848-80
; Sequence 80: Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
```

```
; CURRENT APPLICATION NUMBER: US/10/062.848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 465
; TYPE: PR1
; ORGANISM: Aspergillus fumigatus
; US-10-062-848-80

Alignment Scores:
Pred. No.: 4,54e-146 Length: 465
Score: 1880.00 Matches: 358
Percent Similarity: 84.15% Conservative: 35
Best Local Similarity: 76.66% Mismatches: 72
Query Match: 75.62% Indels: 2
DB: 15 Gaps: 2

US-09-488-265B-30 (1-1404) x US-10-062-848-80 (1-465)
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QY 1 ATGGCGGTGTTGCTGCTGCTACTGTCCATTCGCCACCTTGTTCGGTCCCAICCGGTACC 60
Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 61 GCCTTGGTCTCGTGTAACTCTCACTCTTGTGACACTGTTCACGGTGTGTACCAATGT 120
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 121 TTCACAGAAATTCACACTTGTGGGTACATACTCTCCATCTCTCTTTGGGTCGACGAA 180
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY 181 TCTGCTATTCTCCAGACGCTTCCAAAGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
Db 60 LeuSerValSerSerLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 ACACACGGTGTAGATACCCAACTCTTCTCGGCTCTAAGCGGTACTCTGCTTCAATGAA 300
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99
QY 301 GCTATTCAAAAGAACGCTACTGCTTCAAGGTTAAGTACGCTTCTTCTTGAAGACTTACAAC 360
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 361 TACACTTGGGTGCTGACGACTTGACTCCATTCGCTGACACCAACAAATGGTTAAGCTGGT 420
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAGTCTTACAGAGATACAAAGCTTGGCTAGAAAGATTGTTCATTCATITAGAGCT 480
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 481 TCTGGTCTGACAGAGTTATTGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
QY 541 AAGTTGGCTGACCCAGGTGCTTAACCCACACCAAGCTTCTCCAGTTATTATTAATATT 600
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
QY 601 CCAGAAAGTGTGGTTACAAACAACTTTGGACCAAGGTTTGTGTACTGCTTGTTCGAAGAA 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATTCGGTGACGACTTCAAGCTAACTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATTGGAAGCTCACTTGCCAGGTGTTAACTTGTACTGACGACGAGAGCTGTTGAAC 780
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239	Db	AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu	258
781	Qy	ATGACATGTGTCCATTCCGACTGTGTAGAACTTCTGACGCTACCAATCTCTCCCA	840
259	Db	MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro	275
841	Qy	TTCTCTGACTTGTTCACCTCAGCAGCAATGGATTCANACGACTACTTCGCAATCTTGGT	900
279	Db	PheCysGlnLeuPheThrHisasnGluTrpLysLysIYFasnIYLeuGlnSerLeuGly	298
901	Qy	AACTACTACGGTTACGTTGGTGAACCCATTGGGTCACAGCTCAAGGTTGGTTTCCTT	960
299	Db	LysTyTyTyGlyTyGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr	318
961	Qy	ACGAAATTGANTGTACATTCACCTCACTCTCCAGTTCACAGCCACCACTTCTTAC	1020
319	Db	AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer	338
1021	Qy	ACTTTGGACTCTAACCCAGCTACTTTCCTCCATTGAACGCTACTTGTACGCTGACTTCT	1080
339	Db	ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyValAspPheSer	356
1081	Qy	CACGACAACTATGGTTTCTATTCTTCGCTTGGGTTTGTACAAAGCGTACTAAGCCA	1140
359	Db	HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyAsnGlyThrGluPro	378
1141	Qy	TTGCTACTACTCTGTGTGAATCTATTGAAGAACTGACGGTTACTCTGCTCTCTGGACT	1200
379	Db	LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTySerAlaSerTrpVal	398
1201	Qy	GTTCATCTCGCTCGTACAGCTTACGTTGAAATCATGCATGCAAGCTGAAAGCAACCA	1260
399	Db	ValProPheGlyAlaAlaArgAlaIYrPheGluThrMetGlnCysLysSerGluLysGluSer	418
1261	Qy	TTGGTTAGAGTMTTGGTTAAACACAGAGTTGTTCATTGCAGGGTTGGTGTGTGACAAG	1320
419	Db	LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys	436
1321	Qy	TTGGGTAGATGATAGACAGCAGCTTCGTTGAAGGTTGTCTTCGCTAGATCTGGTGGT	1380
439	Db	LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly	458
1381	Qy	AACTGGGAAGAATGTTTCGCT	1401
459	Db	AsnTrpGlyGluCysPheSer	465

RESULT 7

```

US-10-062-848-79
: Sequence 79, Application US/10062848
: Publication No. US20030092155A1
:
: GENERAL INFORMATION:
:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TONSCHE, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
:
: TITLE OF INVENTION: MODIFIED PHYTASES
:
: FILE REFERENCE: Modified Phytases
:
: CURRENT APPLICATION NUMBER: US/10/062.848
:
: CURRENT FILING DATE: 2002-02-01
:
: PRIOR APPLICATION NUMBER: 09/044,718
:
: PRIOR FILING DATE: 1998-03-19
:
: PRIOR APPLICATION NUMBER: EP 97810175.6
:
: PRIOR FILING DATE: 1997-03-25
:
: NUMBER OF SEQ ID NOS: 82
:
: SOFTWARE: PatentIn ver. 2.1
:
: SEQ ID NO 79
:
: LENGTH: 465
:
: TYPE: PRT
:
: ORGANISM: Aspergillus fumigatus
:
US-10-062-848-79

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Alignment Scores:
 bred. NO.: 5,48e-146 Length: 465
 Score: 1879.00 Matches: 358
 Percent Similarity: 84.15% Conservative: 35
 Best Local Similarity: 76.66% Mismatches: 72
 Query Match: 75.58% Indels: 2
 DB: 15 Gaps: 2

CS-09-488-265B-30 (1-1404) x US-10-062-848-79 (1-465)

QY	1	ATUGGGGTGTTCTCGTGCTAGTGTCCCAITGGCACCTTGTTCGGTTCACATCCGGTACC	60
DB	1	MetValThrLeuThrPheLeuLeuSerAlaAlaIleLeuLeuSerGlyArgValSerAla	20
QY	61	GCCTTGGGTCTCGTGGTAACTCTCACCTCTGTGACACTGTTGACGGTGGTACCAATGT	120
DB	21	AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys	39
QY	121	TTCCAGAAATTTCTCACCATTGGGGGTACATACTCCCATCTCTCTTTGGGTGACGAA	180
DB	40	SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPheSerLeuGluAspGlu	59
QY	181	TCGTCTATTCTCCAGACGTTCCAAAGGGTGTAGAGTACTCTTCGTCACAGTTTGTCT	240
DB	60	LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer	79
QY	241	AGACAGGGTCTAGATACCACTTCTTCTGCGTCTAAGGGGTACTCTGCTTTGATGAA	300
DB	80	ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysIleLysLysLeuValThr	99
QY	301	GCATTCAAAGAACGCTACTCTCTTCAGGGTAGTAGCGTTCTTCAAGACHTACAAAC	360
DB	100	AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn	119
QY	361	TACACTTTGGGTGCTCAGCACTTGACTCCATTCGGGTGAACAACAAATGGTTAATCTGGT	420
DB	120	TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly	139
QY	421	ATTAAGTTCTACAGAGATACAGGCTTTGGGTAGAAAGATTTGTCATTTCATTAGAGCT	480
DB	140	IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla	159
QY	481	TCGTGTTCTCACAGAGTATTGCTTCTCGCTGAAAAGTTTCATTGAAGGTTTCCATCTGCT	540
DB	160	SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAla	179
QY	541	AGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTCTCCAGTATTAAAGCTATTATT	600
DB	180	LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle	199
QY	601	CCAGAAGGTGCTGTTTACAAACACACTTTGGACACCGGTTTGTGTACTGCTTTCCGAAGA	660
DB	199	ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla	218
QY	661	TCGTGAATGGGTGACGACGCTTGAAGCTAACTTCATCTGCTGTTTTCGCTCCACCAATAGA	720
DB	219	SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg	238
QY	721	GCATAGTTGAACTTCACCTTGGCAGGTGTAACTTGACTGACGAGAGCGTTGTAACTTG	780
DB	239	AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu	258
QY	781	ATGACATGTGTCATTCCAGCACTGTGTGCTAGAACTTCTGACGCTACTCAATTCCTCCA	840
DB	259	MetAspMetCysSerPheAspThrValAlaAlaArgThrSerAspAlaSerGlnLeuSerPro	278
QY	841	TTCGTGCACTTGTTCACCTCACGACGAATGGATTTCATACGACTACTTCCAACTCTTGGGT	900
DB	279	PheCysGlnLeuPheThrHisAsnGluThrLysLysTyrAsnIleLeuGlnSerLeuGly	298
QY	901	AAGTACTACGGTTACCGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTGTGTTTCGTT	960


```
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 81
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Alignment Scores:
Pred. No.: 9,68e-146 Length: 465
Score: 1876.00 Matches: 357
Percent Similarity: 84.15% Conservative: 36
Best Local Similarity: 76.45% Mismatches: 72
Query Match: 75.46% Indels: 2
DB: 15 Gaps: 2

US-09-488-265b-30 (1-1404) x US-10-062-848-81 (1-465)

QY 1 ATGGCGGCGTCTGCTGCTACTGCTCCATTCGACCTTGTTCGGTCCACATCCGGTACC 60
Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20

QY 61 GCCTTGGGTCCTCGGTAACTCTACACTCTTGTGACACTGTGACGGTGGTACCAATGT 120
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39

QY 121 TTCCCAAGAAATTCCTCACTTGTGGGTACATCTCCATCTCTCTCTTCTTGGCTGACGAA 180
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59

QY 181 TCTGCTATTCTCCAGACCTCCAAAGGTTGTAGAGTACTTTCGTTCAAGTTTGTCT 240
Db 60 LeuSerValSerLysLeuProLysCysArgIleThrLeuValGlnValLeuSer 79

QY 241 AGACAGGTGCTAGATACCAACTCTCTCTGCGTCTAAGGCTACTCTGCTTTGATTGAA 300
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLysLeuValThr 99

QY 301 GCTATTCAAAGACCTACTCTCTCAAGGTAGTACGCTTCTTGAAGACTTACAC 360
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 159

QY 361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAAATGGTTAACTCTGT 420
Db 120 TyrThrLeuGlyAlaAspAspLeuThrAlaPheGlyGluGlnGlnLeuValAsnSerGly 139

QY 421 ATTAAGTTCTACAGAGATACAGGCTTTGGCTAGAAGATTGTTCCATTTCATTAGACT 480
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

QY 481 TCTGGTCTTCACAGACTTATGCTCTGCTGAAAAGTTCATTGAAGGTTTCCATCTGCT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAla 179

QY 541 AAGTTGGCTGACCCAGGTCTAACCCACACCAAGCTTCTCCAGTTTAAAGCTATTATT 600
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198

QY 601 CCAGAGGTGCTGTTACACACACACTTTGGACCCAGGTTTGTGACTGCTTTCCAGAA 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspPheHisGlyValCysThrLysPheGluAla 218

661 TCTGAATTGGGTGACGAGGTTGAACCTAACTTCACTGCTGTTTTCGGTCCACCAATTAGA 720
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238

721 GCTAGATTGGAAGCTCACITGCCAGGTCTTAACCTTGACTGACGAGGAGCTGTGTTAACTTG 780
Db 239 AlaArgAlaLysLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258

781 ATGGACATGTGTCATTCGACACTTGTCTAGAAGTTCGTGACGCTACTCAATGTCTCCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278

841 TTCTGTGACTTGTTCACCTCAGCACAATGGATTCAATACGACACTTTCACATCTTGGGT 900
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298

901 AAGTACTACGGTTACGGTGTGTAACCCATTGGTCCAGCTCAAGGTGTGTGGTTTCGTT 960
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318

961 AACGAATTGCTAGATTGACTCCTCCTCAGTTCAGGTTCAAGACACACTTCTACTAACCA 1020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338

1021 ACTTTGGACTCTAACCCAGCTACTTTCCTCATTTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358

1081 CACGACACACTATGTTTCTATTTTCTTCGTTTGGGTTTGTACAGGGTACTAAGCCA 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378

1141 TTCTCTACTACTTCTGTTGAATCTATTGAAGAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerIrpVal 398

1201 GTTCCATTGCTGCTAGAGCTTACGTTCAATGATGCAATGTGAAGCTGAAGAGGACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418

1261 TTGGTTAGAGTTTGGTTAACGACAGCTGTCATTGACGCTTGGGTGGTGGTGGTGGT 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438

1321 TTGGGTAGATGTGAAGAGAGACGACTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGT 1380
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458

1381 AACTGGGAGAAGATGTTTCCT 1401
Db 459 AsnTrpGlyGluCysPheSer 465

RESULT 11
US-10-062-848-82
: Sequence 82, Application US/10062848
: Publication No. US20030092155A1
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
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; SEQ ID NO 82
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-82

Alignment Scores:
Pred. No.:      6,27e-144      Length:      469
Score:          1854.00      Matches:      347
Percent Similarity: 84.47%      Conservative: 50
Best Local Similarity: 73.83%      Mismatches: 69
Query Match:      74.58%      Indels:      4
DB:              15      Gaps:      2

US-09-488-265B-30 (1-1404) x US-10-062-848-82 (1-469)

QY      1  ATGGCGGTTCGGTGGTCTACTGTCCTCCACCTGTTGGTTCACATCCGGT--- 57
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      1  MetGlyAlaLeuThrPheLeuSerValMetTyrLeuSerGlyValAlaGlyAla 20

QY      58  -----ACGGCTCGGTCCGGTGAACCTCACCTCTGACACTCTTGACACTGGTTCACCGTGGT 111
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      21  ProSerSerGlyCysSerAlaClySerGlySerLysAlaCysAspThrValGluLeuGly 40

QY      112  TACCAATGTTCCCAAGAAATTCCTACCTGTGGGTACATCTCTCCATTCTCTCTCTG 171
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      41  TyrGlnCysSerProGlyThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeu 60

QY      172  GCTGACGAATCTGCTATTCTCCAGACGCTTCCAAAGGCTTGAGAGTACTTCTGCTCAA 231
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      61  GluAspGluLeuSerValSerSerAspLeuProLysAspCysArgValThrPheValGln 40

QY      232  GTTTGTCTAGACGCGTCTAGATACCACTCTCTGCTGCTTAAGCGCTACTCTGCT 291
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      81  ValLeuSerArgHisGlyAlaArgTyrProThrAlaSerLysSerLysLysTyrLysLys 100

QY      292  TTGATTGAAGCTATTCAAAGAACGCTACTGCTTTCAAGGGTGAAGTCTTCTTGAAG 351
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      101  LeuValThrAlaIleGlnLysAsnAlaThrGluPheLysGlyLysPheAlaPheLeuGlu 120

QY      352  ACTTACACTACACTTGGGTCTGACACTGACTCTCCATTCGGTGAACACAATGGTT 411
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      121  ThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnMetVal 140

QY      412  AACTCTGGTATTAACTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATGTTCCATTC 471
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      141  AsnSerGlyLysPheTyrGlnLysTyrLysAlaLeuAlaGlySerValValProPhe 160

QY      472  ATTAGAGCTTCTGGTCTGACAGAGTTATTGCTTCTGCTGAAAGTTCATTGAAGTTTC 531
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      161  IleArgSerSerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPhe 180

QY      532  CAATCTGCTGAAGTCTGCTGACCGCTGCTAACCACACCAAGCTTCCAGCTTATTAAAC 591
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      181  GlnGlnAlaAsnValAlaAspProGlyAlaThr---AsnArgAlaAlaProValIleSer 199

QY      592  GTATTATTCCAAAGTGTGTTGATCAACACACTTTGGACACCGTTCCTGCTGCTGCT 651
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      200  ValIleProGluSerGluThrTyrAsnAsnThrLeuAspHisSerValCysThrAsn 219

QY      652  TTCGAAGAATCTGAATTGGTGACAGCTTGAAGCTAATCTTCACTGCTGCTTTCGCTCA 711
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      220  PheGluAlaSerGluLeuGlyAspGluValGluAlaAsnPheThrAlaLeuPheAlaPro 239

QY      712  CCAATTAGACTAGATTGGAACCTCACTGCCAGCTGTTAATCTGACTGACCAACAGCTT 771
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      240  AlaIleArgAlaArgIleGluLysHisLeuProGlyValGlnLeuThrAspAspVal 259

QY      772  GTTAACCTGATGACATGTGCTCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAA 831
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      260  ValSerLeuMetAspMetCysSerPheAspThrValAlaArgThrAlaAspAlaSerGlu 279

QY      832  TTGCTCTCCATTCTGTGACTTGTCTACTCACGACGAATGATGATCAATACGACTACTTCAA 891

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Db      280  LeuSerProPheCysAlaIlePheThrHisAsnGluThrPlyLysTyrAspTyrLeuGln 299
QY      892  TCITTTGGGTAAGTACTACGGTTACGGTCTGGTAACCCATTTGGGTCCAGCTCAAGTGTI 951
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      300  SerLeuGlyLysTyrTyrGlyIyrGlyAlaGlyAsnProLeuGlyProAlaGluGlyIle 319

QY      952  GGTTTCGTTAACCAATTTGATGCTAGATGCTACTCTCCAGTTTCAAGACCACACTTCT 1011
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      320  GlyPheThrAsnGluLeuIleAlaArgLeuThrAsnSerProValGlnAspHisThrSer 339

QY      1012  ACTAACCCACACTTTGGACTCTAACCCAGCTACTTCCCATTTGAACGCTACTTGTACGCT 1071
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      340  ThrAsnSerThrLeuAspSerAspProAlaThrPheProLeuAsnAlaThrIleTyrVal 359

QY      1072  GACTTCTCTCAGACACACTACTGGTTTCTATTCTTCTCGCTTTGGGTTTGTACACGGT 1131
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      360  AspPheSerHisAspAsnGlyMetIleProIlePheAlaMetGlyLeuIyrAsnGly 379

QY      1132  ACTAAGCCATTGTCTACTTCTGTAATCTATTGAAGAAACAGAGGTTTACTCTGCT 1191
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      380  ThrGluProLeuSerGlnThrSerGluSerThrLysGluSerAsnGlyTyrSerAla 399

QY      1192  TCTTGGACTGTTCCATTCGCTGCTAGAGCTTACGTTGAATGATGCAATGTGAAGTGAA 1251
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      400  SerTrpAlaValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGlu 419

QY      1252  AAGAACCATTTGGTGTAGAGTTTGGTTTACGACAGAGTGTTCATTCATTCGACGGTGTG 1311
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      420  LysGluProLeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAla 439

QY      1312  GTTCACAAGTTGGGTAGATCTAAGAGAGACGACTTCTGCTCAAGGTTTGTCTTTCGCTAGA 1371
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      440  ValAspLysLeuGlyArgCysLysLeuLysAspPheValLysGlyLeuSerTrpAlaArg 459

QY      1372  TCTTGGTGAAGTGGGGAAGTGTTCGCT 1401
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      460  SerGlyAsnSerGluGlnSerPheSer 469

RESULT 12
US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbia
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510
; FILING DATE: 20-JAN-1999

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221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240

721 GCATAGTTGGAGCTCACITTCGCCAGGTGGTTAACTTGTGACTGACGAAGACGCTGTTAACTTG 780

241 GlnArgLeuGluAsnAspLeuSerGlyValIhrLeuThrAspThrGluValThrIyrLeu 260

781 ATGGACATGTGTCATTCGACATGTTGCTAGNACTTCTGAGCGTACTCAATGTCCTCCA 840

261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280

841 TTTCTGTGACTTGTTCACCTACGACGAGATGCAATTCAGTACTCTTCCAAATCTTTGGGT 900

281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

901 AAGTACTACGGTTACGGTGTGTTACCCATGTCAGCTACTTGTACGCTGACTTCTCTCT 960

301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValClyTyrAla 320

961 AACGAATGATTGCTAGATGACTCACCTCCAGTTCACAGACACACACTTCTACTAACCA 1020

321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspThrSerSerAsnHis 340

1021 ACTTTGGACTCTAACCCAGCTACTTTCCTCCATTAAGCGTACTTGTACGCTGACTTCTCT 1080

341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360

1081 CACGACACACTATGTTGTTCTATTCTTCGCTTGGGTTCGTACAACGGTACTAAGCCA 1140

361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

1141 TTGCTCTACTCTCTGTGTGAATCTATTGAAGAACTGACGGTACTCTGCTTCTTGACT 1200

381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400

1201 GTTCATCTCGCTGTAGAGCTTACGTTGAATCATCAATGTGAAGCTGAAAGGAACCA 1260

401 ValProPheAlaSerArgLeuTyrValGluMetGlnCysGlnAlaGluGlnGluPro 420

1261 TTGGTTAGAGTTTGGTTTACGACAGAGTTGTTCCATTCACGGTGTGCGTGTGTCACAG 1320

421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440

1321 TTGGGTAGATGTAAGACGACGACCTTCGTTGAAGGTTTGTCTTCGTAGACTCTGGTGGT 1380

441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460

1381 ACTCGGGAAGTATGTTCCCT 1401

461 AspTyrAlaGluCysPheAla 467

RESULT 13

US-10-229-358-5

: Sequence 5, Application US/10229358

: Publication No. US20030124700A1

: GENERAL INFORMATION:

: APPLICANT: Stafford, Christian F.

: APPLICANT: Trinci, Anthony P.J.

: APPLICANT: Brookman, Jayne L.

: TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding

: FILE REFERENCE: GC586-2

: CURRENT APPLICATION NUMBER: US/10/229,358

: PRIORITY FILING DATE: 2002-08-26

: PRIOR APPLICATION NUMBER: US 60/148,960

: PRIOR FILING DATE: 1999-08-13

: NUMBER OF SEQ ID NOS: 34

: SOFTWARE: FastSeq for Windows Version 4.0

: SEQ ID NO 5

: LENGTH: 467

: TYPE: PRT

: ORGANISM: Aspergillus niger

US-10-229-358-5

Alignment Scores:

Pred. No.: 1,95e-143 Length: 467
Score: 1848.00 Matches: 347
Percent Similarity: 83.30% Conservative: 42
Best Local Similarity: 74.30% Mismatches: 78
Query Match: 74.34% Indels: 0
DB: 15 Gaps: 0

US-09-488-265B-30 (1-1404) x US-10-229-358-5 (1-467)

QY 1 ATGGGCGTGTTCGTGCTGCTACTGTCATTCGACCTGTTCGGTTCACACCTCTACTACCGTACC 60
DB 1 MetGlyValSerAlaValLeuLeuProLeuTyLeuLeuSerGlyValThrSerGlyLeu 20
QY 61 GCCTTGGGTCCTCGTGGTCACTCTCTGACACTGTTGACGGTGGTGTACCAATGT 120
DB 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTrpGlnCys 40
QY 121 TTCCAGAAATTTCTCAGTTGGGTGATACACTCTCCATCTCTCTTTCGCTCAGCAA 180
DB 41 PheSerGluThrSerHisLeuTrpGlyGlnTyAlaProPhePheSerLeuAlaAsnGlu 60
QY 181 TCTGCTATTCTCCAGACGTTCCAAAGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
DB 61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80
QY 241 AGACGGTGCTAGATACCAACTTCTTCTGGGCTTAAGGGTACTCTGCTTGTATTGAA 300
DB 81 ArgHisGlyAlaArgTyProThrAspSerLysGlyLysLysTySerAlaLeuIleGlu 100
QY 301 GCTATTCAAAGAACGCTACTGCTTTCAGGGTAACTACGTTTCTTGAAGCTTTACAC 360
DB 101 GluIleGlnAsnAlaThrThrPheAspGlyLysTyAlaPheLeuLysThrTyAsn 120
QY 361 TACACTTTGGTCTGACGACTGCTCCATTCGTTGAGTGAACAACAAATGTTAACTCTGT 420
DB 121 TySerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 421 ATTAAGTTCTACAGAGATACAGGCTTTGGGTAGAAAGATTGTTCCATTCAITAGACT 480
DB 141 IleLysPheTyGlnArgTyGluSerLeuThrArgAsnIleValProPheIleArgSer 160
QY 481 TCTGGTCTCACAGATTTATGCTTCTGCTGAAAGTTCAATGAAGTTTCCAAATCTGT 540
DB 161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180
QY 541 AAGTTGGCTGACCGAGTGCTACCCACACCAAGCTTCTCCAGTTATTAACTGTTATTAT 600
DB 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValIle 200
QY 601 CCAGAAGTGCTGTTTACAAACACACTTTGGACCCACGGTTTGTGTACTGCTTCCGAAGA 660
DB 201 SerGluAlaSerSerSerAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY 661 TCTGAATTTGGTGACGAGTTGAAGCTTAATCTACCTGCTGTTTTCGCTCCACCAATTAGA 720
DB 221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
QY 721 GCTAGATTGGAAGCTCACTTGCACGAGTGTAACTTCACTGACGACGACGCTTGAAC 780
DB 241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyLeu 260
QY 781 ATGACATGTTCCATTCGACACTGTTGCTGAGAACATCTGACGCTACTCAATGTCTCCA 840
DB 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
QY 841 TTCGTGACTTGTTCATCTACGAGGAATGATTCATACAGACTACTTGAATCTTTGGGT 900
DB 281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyAspTyLeuGlnSerLeuLys 300
QY 901 AAGTACTACGGTTACGCTGCTGTAACCCATTGGGTCCAGCTCAAGGTGTGCTTTCGT 960
DB 301 LysTyTyGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyAla 320

QY 561 AACGAATGATTGCTAGATTGACTCTCAGTTCAGGCTTCAAGACACACACTTCTACTAACCA 1020
DB 321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspThrSerSerAsnHis 340
QY 1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTTGAAGAACTGACGGTACTCTGCTTCT 1080
DB 341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyAlaAspPheSer 360
QY 1081 CAGCAACACACTATGTTCTATTCTTTCGTTTGGGTTTGTACAAAGGTTACTAAGCCA 1140
DB 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyAsnGlyThrLysPro 380
QY 1141 TTGCTACTACTTCTCTGAACTATTGAAGAACTGACGGTACTCTGCTTCTTGGACT 1200
DB 381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
QY 1201 GTTCCATTGCTGCTAGAGCTTACGTTGAAATGATGCTCAATGTGAAGCTGAAAGCAACA 1260
DB 401 ValProPheAlaSerArgLeuTyValGluMetGlnCysGlnAlaGluGlnGluPro 420
QY 1261 TTGGTTAGAGTTTGGTTAAAGACAGAGTTGTTCATTCACGGTTGTGCTGTTGACAG 1320
DB 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440
QY 1321 TTGGTAGATGTAAGACAGACGACTTCTGTTGAAGTTTCTTTCGCTAGATCTGTTGCT 1380
DB 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGAAGAATGTTTCGCT 1401
DB 461 AspTrpAlaGluCysPheAla 467

RESULT 14
US-09-929-060-3
Sequence 3, Application US/09929060
Patent No. US20020068350A1
GENERAL INFORMATION:
APPLICANT: KONDO, HIROMASA
APPLICANT: ANAZAWA, HIDEHARU
APPLICANT: KANEKO, SYUNICHI
APPLICANT: NAKASHIMA, TADASHI
APPLICANT: TANGE, TATSUYA
TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
FILE REFERENCE: 081356/0166
CURRENT APPLICATION NUMBER: US/09/929,060
PRIOR FILING DATE: 2001-08-05
PRIOR APPLICATION NUMBER: 09/543,744
PRIOR FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: 09/155,855
PRIOR FILING DATE: 1998-10-05
PRIOR APPLICATION NUMBER: JP 084314/1996
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 467
TYPE: PRT
ORGANISM: Aspergillus niger
US-09-929-060-3

Alignment Scores:
Pred. No.: 7,34e-143 Length: 467
Score: 1841.00 Matches: 342
Percent Similarity: 83.73% Conservative: 49
Best Local Similarity: 73.23% Mismatches: 76
Query Match: 74.05% Indels: 0
DB: 9 Gaps: 0

US-09-488-265B-30 (1-1404) x US-09-929-060-3 (1-467)

QY 1 ATGGGCGTGTTCGTGCTGCTACTGTCATTCGACCTGTTCGGTTCACACCTCTACTACCGTACC 60
DB 1 MetGlyValSerAlaValLeuLeuProLeuTyLeuLeuSerGlyValThrSerGlyLeu 20
QY 61 GCCTTGGGTCCTCGTGGTCACTCTCTGACACTGTTGACGGTGGTGTACCAATGT 120
DB 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTrpGlnCys 40
QY 121 TTCCAGAAATTTCTCAGTTGGGTGATACACTCTCCATCTCTCTTTCGCTCAGCAA 180
DB 41 PheSerGluThrSerHisLeuTrpGlyGlnTyAlaProPhePheSerLeuAlaAsnGlu 60
QY 181 TCTGCTATTCTCCAGACGTTCCAAAGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
DB 61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80
QY 241 AGACGGTGCTAGATACCAACTTCTTCTGGGCTTAAGGGTACTCTGCTTGTATTGAA 300
DB 81 ArgHisGlyAlaArgTyProThrAspSerLysGlyLysLysTySerAlaLeuIleGlu 100
QY 301 GCTATTCAAAGAACGCTACTGCTTTCAGGGTAACTACGTTTCTTGAAGCTTTACAC 360
DB 101 GluIleGlnAsnAlaThrThrPheAspGlyLysTyAlaPheLeuLysThrTyAsn 120
QY 361 TACACTTTGGTCTGACGACTGCTCCATTCGTTGAGTGAACAACAAATGTTAACTCTGT 420
DB 121 TySerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 421 ATTAAGTTCTACAGAGATACAGGCTTTGGGTAGAAAGATTGTTCCATTCAITAGACT 480
DB 141 IleLysPheTyGlnArgTyGluSerLeuThrArgAsnIleValProPheIleArgSer 160
QY 481 TCTGGTCTCACAGATTTATGCTTCTGCTGAAAGTTCAATGAAGTTTCCAAATCTGT 540
DB 161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180
QY 541 AAGTTGGCTGACCGAGTGCTACCCACACCAAGCTTCTCCAGTTATTAACTGTTATTAT 600
DB 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValIle 200
QY 601 CCAGAAGTGCTGTTTACAAACACACTTTGGACCCACGGTTTGTGTACTGCTTCCGAAGA 660
DB 201 SerGluAlaSerSerSerAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY 661 TCTGAATTTGGTGACGAGTTGAAGCTTAATCTACCTGCTGTTTTCGCTCCACCAATTAGA 720
DB 221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
QY 721 GCTAGATTGGAAGCTCACTTGCACGAGTGTAACTTCACTGACGACGACGCTTGAAC 780
DB 241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyLeu 260
QY 781 ATGACATGTTCCATTCGACACTGTTGCTGAGAACATCTGACGCTACTCAATGTCTCCA 840
DB 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
QY 841 TTCGTGACTTGTTCATCTACGAGGAATGATTCATACAGACTACTTGAATCTTTGGGT 900
DB 281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyAspTyLeuGlnSerLeuLys 300
QY 901 AAGTACTACGGTTACGCTGCTGTAACCCATTGGGTCCAGCTCAAGGTGTGCTTTCGT 960
DB 301 LysTyTyGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyAla 320

Db 1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20
QY 61 GCCTTGGCTCTCGTGGTAACTCTCACTCTGTGACACGTGTGACGGTGGTACCAATGT 120
Db 21 AlaValProAlaSerArgAsnGlnSerThrCysAspThrValAspGlnGlyTyrGlnCys 40
QY 121 TTCACAGAAATTTCTCACTCTGTGGGTACATCTCACTCTGTCTCTGTGGCTGACGAA 180
Db 41 PheSerGlnThrSerHisLeuTyrGlyGlnTyrAlaProPhePheSerLeuAlaAsnLys 60
QY 191 TCTGCTATTTCTCAGACGTTCCAGGGTGTAGAGTTACTTCTGTCAGATTTTGTCT 240
Db 61 SerAlaIleSerProAspValProAlaGlyCysHisValThrPheAlaGlnValLeuSer 80
QY 241 AGACACGGTGTAGATACCCAACTTCTCTCGCTCTAAGCGGTACTCTCTGTGATGAA 360
Db 81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
QY 301 GCTATTCAGAGACGCTACTGCTTTCAGGGTAAAGTACGCTTCTTCAAGCTTACAC 360
Db 101 GluIleGlnGlnAsnAlaThrThrPheGluGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 361 TACACTTGGTGTGCTGACGCTTCACTCCATTCGCTGACCAACAAATGTTCAACTCTGT 420
Db 121 TyrSerLeuGlyAlaAspLeuThrProPheGlyGlnGlnLeuValAsnSerGly 140
QY 421 ATTAGTCTACAGACGCTTCAAGGCTTGGCTAGAAGATTGTTCCATTCATTAGCT 480
Db 141 ValLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160
QY 481 TCTGCTCTGACAGATATTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 161 SerGlySerSerArgValIleAlaSerGlyAsnLysPheIleGluGlyPheGlnSerThr 180
QY 541 AGTTGGCTGACCGAGTGTACCCACACGCTTCCAGCTTCCAGCTTATTAAT 500
Db 181 LysLeuLysAspProArgAlaGlnProGlyLysSerSerProLysIleAspValValle 200
QY 601 CCAGAGGTGTGCTTCAACACACACTTGCACACGCTTGTGCTGCTGCTGCTGCTGCTGCT 660
Db 201 SerGluAlaSerThrSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY 661 TCTGAATGGGTGACGAGTGTGAGCTTAACCTCACTCTGTTTCTGCTCCACCAATAGA 720
Db 221 SerGluLeuAlaAspAspIleGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
QY 721 GCTAGATTGGAAGCTCACTTCCAGGTGTTAACTTGACTGACGACGAGCTGTAACTTG 780
Db 241 GlnArgLeuGluAsnAspLeuSerGlyValSerLeuThrAspThrGluValThrTyrLeu 260
QY 781 ATGGACATGTGCTCACTGACGAGTGTGCTAGAACITCTGACGCTACTCAATGTCTCA 840
Db 261 MetAspMetCysSerPheAspThrIleSerThrValAspThrLysLeuSerPro 280
QY 841 TCTGTGACTTGTTCACACGAGATGGAATCAATACGACTTGTGCAATCTTGGT 900
Db 281 PheCysAspLeuPheThrHisGluGluTyrIleAsnTyrAspTyrLeuGlnSerLeuAsn 300
QY 901 AAGTACTAGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
QY 961 AACGAATGATTGCTAGATTCACCTCTCCAGTTCAGGACGACCTTCTACTAACCA 1020
Db 321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspThrSerSerAsnHis 340
QY 1021 ACTTTGGACTCTAACCCAGCTACTTCCATTAAGCTACTTGTGACGCTGCTCTCT 1080
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QY 1141 TTGCTACTACTTCTGTTGAATCTTGAAGAACTGACGCTTACTGCTCTGCTGACT 1200
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QY 1321 TTGGTAGATGTAAAGACGACGACTTCCGTTGAAGGTTTGTCTTTCGCTAGATCTGTTGGT 1380
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US-10-083-452-11
: Sequence 11, Application US/10083452
: Publication No. US20020127218A1
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: TITLE OF INVENTION: Phytase Variants
: FILE REFERENCE: 5618-500-US
: CURRENT APPLICATION NUMBER: US/10/083,452
: CURRENT FILING DATE: 2002-02-26
: PRIOR APPLICATION NUMBER: US/09/273,871
: PRIOR FILING DATE: 1999-03-22
: PRIOR APPLICATION NUMBER: PA 1998 00407
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: PA 1998 00806
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: PA 1998 01176
: PRIOR FILING DATE: 1998-09-18
: PRIOR APPLICATION NUMBER: PA 1999 00091
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/080,129
: PRIOR FILING DATE: 1998-03-31
: PRIOR APPLICATION NUMBER: 80/090,675
: PRIOR FILING DATE: 1998-06-25
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 11
: LENGTH: 467
: TYPE: PRT
: ORGANISM: Aspergillus ficuum
US-10-083-452-11

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Score: 1836.00 Matches: 345
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Best Local Similarity: 73.88% Mismatches: 80
Query Match: 73.85% Indels: 0
DB: 14 Gaps: 0

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Db 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40
QY 121 TTCACAGAAATTTCTCACTTGTGGGTGACATCTCTCAATCTTCTTTCGCTGACGAA 180
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GenCore version 5.1.i.6
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Run on: October 3, 2003, 07:48:21 : Search time 21.0567 Seconds
(without alignments)
5642.336 Million cell updates/sec

Title: US-09-488-265B-30

Perfect score: 2486

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Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB-Issued_Patents_AA -QFMT-fastan -SUFFIX-oct3.ra1 -MINMATCH=0.1 -LOOPCL-0
-LOOPEXT=0 -UNITS-bits -START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
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Database : Issued_Patents_AA.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2308	92.8	467	4	US-09-273-871A-9
2	2182	87.8	441	3	US-09-121-425-1
3	2182	87.8	441	3	US-09-634-493A-1
4	2170	87.3	467	3	US-09-121-425-2
5	2170	87.3	467	4	US-09-634-493A-2
6	1888	75.9	465	3	US-08-868-435-33
7	1888	75.9	465	4	US-08-744-231-33
8	1888	75.9	465	4	US-09-044-718-78
9	1888	75.9	465	4	US-09-636-499-6
10	1888	75.9	465	4	US-09-273-871A-8
11	1880	75.6	465	4	US-09-044-718-80
12	1879	75.6	465	4	US-09-044-718-79

13	1878.5	75.6	439	4	US-09-044-718-3	Sequence 3, Appli
14	1878.5	75.6	449	4	US-09-044-718-12	Sequence 12, Appl
15	1876	75.5	465	4	US-09-044-718-81	Sequence 81, Appl
16	1854	74.6	469	4	US-09-044-718-82	Sequence 82, Appl
17	1852	74.5	467	1	US-07-923-724-8	Sequence 8, Appli
18	1852	74.5	467	2	US-08-609-426A-8	Sequence 8, Appli
19	1852	74.5	467	2	US-08-374-652C-2	Sequence 2, Appli
20	1848	74.3	467	1	US-08-151-574-32	Sequence 32, Appl
21	1848	74.3	467	1	US-08-146-424-20	Sequence 20, Appl
22	1848	74.3	467	1	US-08-693-709-2	Sequence 2, Appli
23	1848	74.3	467	1	US-08-419-448-32	Sequence 32, Appl
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26	1848	74.3	467	3	US-09-233-510-32	Sequence 32, Appl
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37	1806	72.6	444	4	US-09-044-718-1	Sequence 1, Appli
38	1804.5	72.6	463	3	US-08-868-435-29	Sequence 29, Appl
39	1804.5	72.6	463	4	US-08-744-231-29	Sequence 29, Appl
40	1804.5	72.6	463	4	US-09-273-871A-10	Sequence 10, Appl
41	1799	72.4	443	3	US-09-155-855-1	Sequence 1, Appli
42	1799	72.4	443	4	US-09-543-744-1	Sequence 1, Appli
43	1799	72.4	443	4	US-09-929-060-1	Sequence 1, Appli
44	1794	72.2	443	3	US-09-155-855-2	Sequence 2, Appli
45	1794	72.2	443	4	US-09-543-744-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

US-09-273-871A-9

; Sequence 9, Application US/09273871A

; Patent No. 6514495

; GENERAL INFORMATION:

; APPLICANT: Svendsen, Allan

; TITLE OF INVENTION: Phytase Variants

; FILE REFERENCE: 5618.500-US

; CURRENT APPLICATION NUMBER: US/09/273,871A

; CURRENT FILING DATE: 1999-03-22

; PRIOR APPLICATION NUMBER: PA 1998 00407

; PRIOR FILING DATE: 1998-03-23

; PRIOR APPLICATION NUMBER: PA 1998 00806

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: PA 1998 01176

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: PA 1999 00091

; PRIOR FILING DATE: 1999-01-22

; PRIOR APPLICATION NUMBER: 60/080,129

; PRIOR FILING DATE: 1998-03-31

; PRIOR APPLICATION NUMBER: 60/090,675

; PRIOR FILING DATE: 1998-06-25

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 467

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Variation

US-09-273-871A-9

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Pred. No.: 7.66e-218

Score: 2308.00

Percent Similarity: 95.72%

Length: 467

Matches: 436

Conservative: 11


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Db 81 ThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100
QY 379 GACTTGACTCCANTTCGGTGAACAACAATGGTTAACTCTGGTATTAACTTCTACAGAAGA 438
Db 101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPheTyrArg 120
QY 439 TACAAGGCTTTCGGCTAGAAAGATTCTCCATTCATTAGAGCTTCTGCTTCTGACAGACTT 498
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QY 619 AACACACTTTTGGACACCGGTTTGTGTACTGCTTTTCGAAGAATCTGAATTCGGTGACGAC 678
Db 181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200
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: Patent No. 6579975
: GENERAL INFORMATION:
: APPLICANT: Lehmann, Martin
: TITLE OF INVENTION: Consensus Phytases
: FILE REFERENCE: consensus phytases 13239
: CURRENT APPLICATION NUMBER: US/09/634.493A
: CURRENT FILING DATE: 2000-08-08
: PRIOR APPLICATION NUMBER: US/09/121.425
: PRIOR FILING DATE: 1998-07-23
: PRIOR APPLICATION NUMBER: EPO 97112688.3
: PRIOR FILING DATE: 1997-07-24
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 441
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:consensus
US-09-634-493A-1

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Percent Similarity: 95.46% Conservative: 11
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Query Match: 87.77% Indels: 0
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; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: Consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634,493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121,425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: consensus
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US-09-634-493A-2
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Pred. No.: 2,69e-204 Length: 467
Score: 2170.00 Matches: 416
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Query Match: 87.29% Indels: 40
Db: 4 Gaps: 2

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QY 121 TCCAGAAATTTCTACITGTCGGGTACATCTCTCCATCTTCTCTTGGCTGACGAA 180
Db 41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60
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Db 61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80
QY 241 AGACACGGTGTAGATACCCAACTTCTTCTGCGCTTAAGCGGTACTCTGCTTTGATTGAA 300
Db 81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla----- 97
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Db 96 -----ThyTrpAsp 100
QY 361 TACACTTTGGTGTGTCAGGACTTGACTCCATTCGCTCAACAAACAAATGCTTAACCTGTGT 420
Db 101 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120
QY 421 ATTAAGTCTTACACAAAGATACAAAGCTTTGGCTAGAAGATTGTTCCATTCATTAGAGCT 480
Db 121 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 140
QY 481 TCTGGTCTGACAGATTATGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160
QY 541 AAGTTGGTGACCCAGGTGCTTAACCCACACCAAGCTTCTCCAGTTATTAAAC----- 591
Db 161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180
QY 592 -----GTTATTATT 600
Db 181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200
QY 601 CCAGAAGGTGCTGTTTACAAACACACTTTGGACACAGCTTTGCTGCTGCTTTCGAGAA 660
Db 201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220
QY 661 TCTGAATTGGGIGACGAGCTTGAAGCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 221 SerGluLeuGlyAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
QY 721 GCTAGATTGAAGCTCACTTCCAGCTGTTAACTTCACTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260
QY 781 ATGCACATGTCTCCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATGTCTCCA 840
Db 261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280
QY 841 TTCTGTGACTTGTCTACTCAGCAGCAATGATTCATACGACTACTTGCATCTTTGGT 900
Db 841 -----
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Db 281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnIleAspTyrLeuGlnSerLeuGly 300
QY 901 AAGTACTACGGITACGGTCTGCTGTAACCCATTGGTCCACCTCAAGGTTGGTTTCGTT 360
DB 301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320
QY 961 AACGAATGATTGCTAGATGACTCTCTCCAGTTCACGACACACACTCTCTACTAACCCAC 1020
DB 321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340
QY 1021 ACTTTGGACTTACCAGCTACTTTCCCATTTGAAGCTACTTTGACGCTGACTTCTCT 1080
DB 341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360
QY 1081 CACCACACACTATGGTTTCTATTTCTTCGCTTTGGGTTTGACACGCTACTTAAGCCA 1140
DB 361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380
QY 1141 TTGTCTACTACTTCTGTTGAATCTATTGAAGAAGTACGCTTACTCTGCTTCTTGCACT 1200
DB 381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpIle 400
QY 1201 GTTCATTCGCTGCTAGCTAGCTTACGTTGAATGATGCAATGTCAGCTGAAGAGACCA 1260
DB 401 ValProPheGlyAlaArgAlaTyrValGluMetGlnCysGlnAlaGluLysGluPro 420
QY 1261 TTGGTTAGAGTTTGGTTAACGACAGAGAGTGTTCCTTCACGCTTGTGGTGTGACAAG 1320
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QY 1321 TTGGTTAGAGTTAGAGAGAGCTTGGTTGAAGGTTTGTCTTCGCTAGATCTGTTGT 1380
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RESULT 6

US-08-868-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221
; GENERAL INFORMATION:
; APPLICANT: Van Loon, Adolphus
; APPLICANT: Mitchell, David
; TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/868.435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/744,231
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: Case Docket 9339
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-2363

Alignment Scores:
Pred. No.: 1.29e-176 Length: 465
Score: 1888.00 Matches: 359
Percent Similarity: 84.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
DB: 3 Gaps: 2

US-09-488-265B-30 (1-1404) x US-08-868-435-33 (1-465)

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QY 301 GCTATTCAAAGACGCTACTGCTTTCAGGGTGAAGTACGCTTCTTTCGAGACTTACAAC 360
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QY 361 TACACTTTGGTGTGACGACTTGCCTCATTCGTTGAGCAACAAGTGTAACTCTGCT 420
DB 120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
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QY 1021 ACTTTGGACTTAACCCAGCTACTTTCCTATTTCTTCCATGACGCTACTTGTACGCTGACTTCTCI 1080
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1081 CACGACACACTATGCTTCTATTTCTTCTTCGCTTGGGTTGTACACGGTACTAAACCA 1140
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QY 1321 TTGGGTAGATGTAAAGACAGACACTCTGCTGAAGGTTTGTCTTTCGCTAGATCTGGTGT 1380
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RESULT 7

US-08-744-231-33

; Sequence 33, Application US/08744231

; Patent No. 6358722

; GENERAL INFORMATION:

; APPLICANT: Van Loon, Adolphus

; APPLICANT: Mitchell, David

; TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY

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NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/744,231
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,757
FILING DATE: 18-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
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FEATURE:
NAME/KEY: misc_feature
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LOCATION: 374
OTHER INFORMATION: /note="potential N-glycosylation site"
US-08-744-231-33
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Alignment Scores:
Pred. No.: 1,29e+176 Length: 465
Score: 1888.00 Matches: 359
Percent Similarity: 84.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
DB: 4 Gaps: 2
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US-09-488-265B-30 (1-1404) x US-08-744-231-33 (1-465)

QY 1 ATGGGCGGTGTTGCTGCTGCTACTGTCATTTGCCACCTTGTTCGTTCCACATCCGGTACC 60

Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20


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QY 541 AAGTGGCGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGCTATTAAAGCTATTAT 603
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QY 601 CCAGAAGTGTGCTTTACAACAACACACTTTGGACACACGGTTTGTGTACTGTTTCGAAGAA 560
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATGGGTGACGACGCTTGAGCTGAAGCTTCTACTCTCTCTTTCGCTCCACCAATAGA 720
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATGGAAGCTCACTCCAGCTGTTAACTTGACTGACGAAGACGCTGTGTAACITG 780
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGACATGTCTCCATCGACACTGTTGTGTAGAACTTCTGACGCTACTCAATTTGCTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TTCTGTGACTTGTTCACCTACGACGAATGGATTCAATACGACTACTTGCATTTGGCT 900
Db 279 PheCysGlnLeuPheThrHisAsnGluThrLysLysThrAsnTyrLeuGlnSerLeuGly 298
QY 901 AAGTACTACGTTTACGTTGTGTAACTTGGCTCCAGCTCAAGCTGTGTGTTTGT 960
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QY 1321 TTGGTAGATGTAAGAGACGACTTCGTTGAAGTTTGTCTTTCGCTAGATCTGCTGT 1380
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RESULT 10

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US-09-273-871A-8
; Sequence 8, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618,500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1998-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
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; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 465
; TYPE: BMT
; ORGANISM: Aspergillus fumigatus
US-09-273-871A-8

Alignment Scores:
Pred. No.: 1,296-176 Length: 465
Score: 1688.00 Matches: 359
Percent Similarity: 84.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
DB: 4 Gaps: 2
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US-09-488-265B-30 (1-1404) x US-09-273-871A-8 (1-465)

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Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPhenThrAlaLeuPheAlaProAspIleArg 238
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RESULT 11

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; Sequence 80, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044, 718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus

US-09-044-718-80

Alignment Scores:

Pred. No.: 7,87e-176 Length: 465
Score: 1880.00 Matches: 358
Percent Similarity: 84.15% Conservative: 35
Best Local Similarity: 76.66% Mismatches: 72
Query Match: 75.62% Indels: 2
DB: 4 Gaps: 2

US-09-488-265B-30 (1-1404) x US-09-044-718-80 (1-465)

QY 1 ATGGCGGTGTCGTCGTCIACCTGCCATTGCCACCTGTTCGGTCCACATCCGGTACC 60
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QY 121 TTCACAGAAATTTCTCACTTGTGGGTGATACATCTCCATCTCTCTTTGGCTGACGAA 180
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Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY 181 TCTGCTATTCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
||||| ||||||||||| ||||||||||| ||||||||||| |||||||
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 AGACACGGTGTAGATACCCCAACTTCTTCTCGCTTAAGCGGTACTCTGCTTTGAATTGAA 300
||||| ||||||||||| ||||||||||| ||||||||||| |||||||
Db 80 ArgHisGlyAlaArgTyrProThrSerLysSerLysLysTyrLysLysLeuValThr 99
QY 301 GCTATTCAAAACAGCGTACTGCTTCAAGGGTAGTACGCTTCTTGAACACTTCAAC 360
||||| ||||||||||| ||||||||||| ||||||||||| |||||||
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACAAACAAATGGTTAACTCGT 420
||||| ||||||||||| ||||||||||| ||||||||||| |||||||
Db 120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAGTTCTACAGAAGATACAGGCTTTGCTGCTAGAAGATTGTTCATTCATTAGAGCT 480
||||| ||||||||||| ||||||||||| ||||||||||| |||||||
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 481 TCTGTTCTGACAGAGTTATTGCTTCTCTGCTGAAAGTTCATTGAAGTTTCCCACTCTCT 540
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Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGluAla 179
QY 541 AAGTTGGCTGACCCAGGTGCTAACCCACCAAGCTTCTCCAGTTATTAACTGTTATTAT 600
||||| ||||||||||| ||||||||||| ||||||||||| |||||||
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
QY 601 CCAGAAGGTGCTGGTTACAACAACACTTGGACACAGGTTTGTGCTGCTTCCGAGAA 660
||||| ||||||||||| ||||||||||| ||||||||||| |||||||
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysIleThrLysPheGluAla 218
QY 661 TCTGAATTGGGTGACGAGCTTGAAGCTTAACCTGCTGCTGTTTTCGGTCCACCAATTAGA 720
||||| ||||||||||| ||||||||||| ||||||||||| |||||||
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATTGGAAGCTCACTTCCAGGTGTTAACTTGACAGGAGAGCGTTGTTAACTTG 780
||||| ||| ||||||||||| ||||||||||| ||||||||||| |||||||
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValSerLeu 258
QY 781 ATGGACATGTGTCCATTGACACTGTTGCTAGAACTTCTGACGCTACTCAATTGCTCCA 840
||||| ||||||||||| ||||||||||| ||||||||||| |||||||
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TTCGTGACTTGTTCACCTCAGCAGGAATGGATTCAATACGACTACTTGCATCTTTGGGT 900
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Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298
QY 901 AAGTACTACGGTTACGGTGTGTTAAACCATTTGGTCCAGCTCAAGGTGTTGTTTCGTT 960

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Db      299  LysTyrTyGlyTyGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
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QY      961  AACGAATTGATGTAGATTACTACTCTCCAGTTCAAGACACACACTTCTACTTAACCAC 1020
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Db      319  AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
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QY      1021 ACTTTGGAGCTTAACCCAGCTACTTCCATTGACCGTACTTGTACGGTGAATTCCT 1080
      |||
Db      339  ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyValAspPheSer 358
      |||
QY      1081 CAGGACACACTATGTTCTTCTATTCTTCCTGTTGGTTGTACAACGGTACTTAAGCCA 1140
      |||
Db      359  HisAspAsnSerMetValSerIlePheAlaLeuGlyLeuTyArgGlyThrGluPro 378
      |||
QY      1141 TTGTCTACTACTTCTGTGAATCATATTGAAGAACTGACGGTACTTGTGTCTTCTGACT 1200
      |||
Db      379  LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTySerAlaSerTrpVal 398
      |||
QY      1201 GTTCCATTGGCTGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGTGAAGGAACCA 1260
      |||
Db      399  ValProPheGlyAlaArgAlaTyPheClnThrMetCnLysLysSerGluLysGluSer 418
      |||
QY      1261 TTGGTTAGAGTTTGGTTAAACACAGAGCTTGTTCATGTGCACGGTTGTGGTGTGACAAG 1320
      |||
Db      419  LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
      |||
QY      1321 TTGGGTAGATGTAAGAGACAGACTTCCTGTTGAAGGTTTGTCTTCCTGCTAGATCTGGT 1380
      |||
Db      439  LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
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QY      1381 AACTGGGAAGAATGTTTCGCT 1401
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Db      459  AsnTrpGlyGluCysPheSer 465
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RESULT 12

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US-09-044-718-79
; Sequence 79, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 79
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-79
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Alignment Scores:

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Pred. No.: 9,86e-176 Length: 465
Score: 1879.00 Matches: 358
Percent Similarity: 84.15% Conservative: 35
Best Local Similarity: 76.66% Mismatches: 72
Query Match: 75.58% Indels: 2
DB: 4 Gaps: 2
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US-09-488-265B-30 (1-1404) x US-09-044-718-79 (1-465)

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QY      1  ATGGGGGTGTTCTGCTGCTGCTACTGTCCATTGCGACCTTGTTCGGTTCCACATCCGGTACC 60
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Db      1  MetValThrLeuThrPheLeuLeuSerAlaAlaTyLeuLeuSerGlyArgValSerAla 20
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QY      61  GCCTTGGGCTCTCGTGGTAACTCTACTCTTGTGACACTGTGTGACGGTGGTTACCAATGI 120
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Db      21  AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyArgLysCys 39
      |||
QY      121  TTCCAGAAATTTCTCACTTGTGGGGTACATACTCTCATCTCTCTCTCTTGGGTGACGAA 180
      |||
Db      40  SerProAlaThrSerHisLeuTrpGlyGlnTrpSerProPheSerLeuGluAspGlu 59
      |||
QY      181  TCIGCTATTTCCTCCAGACGTTCCAAAGGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
      |||
Db      60  LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
      |||
QY      241  AGACACGGTGTAGATACCCCAACTTCTCTCGCTCTAAGCGGTACTCTGCTTGCATTGAA 300
      |||
Db      80  ArgHisGlyAlaArgTyProThrSerSerLysSerLysLysTyLysLysLeuValThr 99
      |||
QY      301  GCTATTCAAAAGACGCTACTGCTTTCAAGGGTAAAGTACGCTTCTTTGAAGACTTACAAC 360
      |||
Db      100  AlalIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyAsn 119
      |||
QY      361  TACATTTGGTGTGTCAGACTTGACTCCATTCGCTGGAACCAACAAATGGTTAACTCTGGT 420
      |||
Db      120  TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
      |||
QY      421  ATTAAGTTCTCAGAGATACAGAGCTTTGGCTAGAAGATTGTTCGATTCATTAAGAGCT 480
      |||
Db      140  IleLysPheTyGlnArgTyLysAlaLeuAlaArgSerValValProPheIleArgAla 159
      |||
QY      481  TCTGTTCTCAGACAGATTATTCCTTCTCTCTGCTGAAAAGTTTCATTGAAGTTTCCAATGCT 540
      |||
Db      160  SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAla 179
      |||
QY      541  AAGTTGGTGCACCCAGGTGCTTAACCCACACCAAGCTTCCAGTTTAAAGCTTAATATT 600
      |||
Db      180  LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIle 198
      |||
QY      601  CCAGAAAGTGTGCTGTTTACAACACACTTTGGACCCAGGTTTGTGTTGTTCTGCTTCCAGAA 660
      |||
Db      199  ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
      |||
QY      661  TCTGAATTTGGTGCAGACGTTGAACTTAACCTTCACTGCTGTTTTCGCTCCCAATTAGA 720
      |||
Db      219  SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
      |||
QY      721  GCTAGATTGGAAGCTCACTTGCAGGTGTAACTTGACTGACGACGAGCGTGTGAACCTG 780
      |||
Db      239  AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
      |||
QY      781  ATGGACATGTGTCATTTCGACACTGTTCCTAGAAGTTCTGACGCTACTCAATTTGCTCCA 840
      |||
Db      259  MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
      |||
QY      841  TTCCTGTGACTTGTTCACCTCAGCAGCAATGGATTCAATACGACTACTTCGCAATCTTGGT 900
      |||
Db      279  PrecysGlnPheThrHisAsnGlnTrpLysTyArgLysLysTyArgLysLysLeuGly 298
      |||
QY      901  AAGTACTACGGTTACGGTCTGTTAACCCATTGGTCCAGCTCAAGGTGTTGGTTTGGT 960
      |||
Db      299  LysTyTyTyGlyTyGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
      |||
QY      961  AACGAATTGATGTAGATTGACTCTACTCTCCAGTTCAAGACACACACTTCTACTTAACCAC 1020
      |||
Db      319  AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
      |||
QY      1021 ACTTTGGAGCTTAACCCAGCTACTTTCGCTTGAAGCGTACTTGTACGGTGAATTCCT 1080
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Db      339  ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyValAspPheSer 358
      |||
QY      1081 CAGGACACACTATGTTTCTATTCTTCTGCTTGGTTTGTACACGGTACTTAAGCCA 1140
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Db      359  HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyArgGlyThrGluGly 378
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QY 1141 TTGCTACTACITCTGTGTGAATCAIATGAAGAAACGACGGTACTCTCTCTCTTGGACT 1200
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Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTy-SerAlaSerTrpVal 398
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QY 1201 GTTCCATTCCCTAGCAGTTACGTTGAATCATCAATGTGAAGCTCAAAAGAACCA 1260
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Db 399 ValProPheGlyAlaArgAlaIlePheGluThrMetGlnCysSerGluGluPro 418
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QY 1261 TTGGTTAGACTTTTGGTTAAGCAGAGAGTTGTTCCTATGCACGGTTGTGGTTGACAAG 1320
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Db 419 LeuValArgAlaLeuLeuAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
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QY 1321 TTGGTTAGAGTTAAGCAGAGACTTCGTTGAGGTTTGTCTTCCTAGACTGGTGGT 1380
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
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QY 1381 AACTGGGAAGAATGTTTCGT 1401
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Db 459 AsnTrpGlyGluCysPheSer 465
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RESULT 13
US-09-044-718-3
; Sequence 3, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREMA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-3

Alignment Scores:
Pred. No.: 1,07e-175 Length: 439
Score: 1878.50 Matches: 351
Percent Similarity: 87.73% Conservative: 35
Best Local Similarity: 79.77% Mismatches: 53
Query Match: 75.56% Indels: 1
DB: 4 Gaps: 1

US-09-488-265b-30 (1-1404) x US-09-044-718-3 (1-439)
QY 82 TCTCACTCTGTGACACTGTGTGACGGTGTACCAATGTTCCAGAAATTTCTCACTTG 141
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Db 1 SerLysSerCysAspThrValAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeu 20
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
QY 142 TGGGGTACATACCTCCATCTCTCTCTTGGCTGACGAATCTGCTATTCTCCAGACGTT 201
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Db 21 TrpGlyGlnThrSerProPhePheSerLeuGluAspGluLeuSerValSerLysLeu 40
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
QY 202 CCAAGGGTTAGAGTTACTTTCGTTCAAGTTTGTCTAGACACGGTGTCTAGATACCCA 261
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Db 41 ProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyAlaArgTyrPro 60
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QY 262 ACTTCTCTCGCTTAAGCGCTACTCTGCTTGTGATCAACCTATTCAAAAGACGCTACT 322
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Db 61 ThrSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 80
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
QY 322 GCTTTCAGGGTAAGTACGGTTTCTTCAAGACTTACAACCTACACTTGGGTGCTGACGAC 381
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Db 82 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnIleThrLeuGlyAlaAspAsp 100
QY 382 TTCACTCCATTCGGTGAACAACAATAGTTTAACTCTGGTATTAAAGTTCTACAGAATAC 441
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Db 101 LeuThrProPheGlyGluGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 120
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QY 442 AAGCTTTGGCTAGAAAGATTGTTCATTCATTAGAGCTTCTGGTCTCAGACAGATTAT 501
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Db 121 LysAlaLeuAlaArgSerValProPheIleArgAlaSerGlySerAspArgValIle 140
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QY 502 GCTTCTCTCTCAAAAGTTTCATTGAAGTTTCCAAATCTGCTAAGTTGCTGACCCAGCTGT 561
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Db 141 AlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaAspProGlyAla 160
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QY 562 AACCACACCAAGCTTCTCCAGTTATTACGTATTATTCATCCAGAAAGTGTCTGGTTACAC 621
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Db 161 Thr---AsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 179
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QY 622 AACACTTTGGACACCGTTTGTGTACTGCTTCCGAAGAATCTCAATTTGGTGGTACGAGCTT 681
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Db 180 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 199
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QY 682 GAAGCTAACTTCACCTGCTGTTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCACTTG 741
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Db 200 AlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAlaArgAlaGluLysHisLeu 219
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QY 742 CCAGTGTTAACCTGACTGACGAGACGGTTGTTAACTTGTATGTCACATGTTCCATTCGAC 801
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Db 220 ProGlyValThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAsp 239
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QY 802 ACTGTTGCTAGAACTTCTGACGCTACTCAATTTGCTCCATCTCTGCTGCTGCTGCTGCTGCT 861
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Db 240 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 259
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QY 862 GACGAATGGATTCAATACGACTACTTCCAAATCTTGGTAAGTACTACGGTTACGGTGT 921
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Db 260 AsnGluTrpLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAla 279
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QY 922 GGTAAACCATTTGGTCCAGCTCAAGGTGTTGTTGTTTAAACCAATTTGTTGCTAGATTG 981
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Db 280 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuAlaArgLeu 299
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QY 982 ACTCACTCTCCAGTTCAAGACCACTTCTACTAACCACACTTTGGACCTTACACCCAGCT 1041
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Db 300 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 319
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QY 1042 ACTTCCCATTTGACGCTACTTGTACGCTGACTCTCTCCAGACACACTATGTTCTTCT 1101
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Db 320 ThrPheProLeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSer 339
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QY 1102 ATTTTCTCGCTTTGGGTTTGTACACGGTACTAAGCCATTGCTACTACTTCTCTGTGAA 1161
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Db 340 IlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgTrpSerValGlu 359
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QY 1162 TCTATTGAAGAACTGACGGTTACTCTGCTCTTGTGACTGTTCCATTCGCTCTAGAGCT 1221
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
Db 360 SerAlaLysGluLeuAspGlyTyrSerAlaSerTrpValValProPheGlyAlaArgAla 379
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
QY 1222 TACGTTCAATGTCAATGTGAAGCTCAAAAGCAACCAATGCTTAGAGCTTTGGTTAAC 1281
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Db 380 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 399
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QY 1282 GACAGAGTTGTTCCATTCGACGGTTGTGGTGTGACAAAGTTGGTGGTGAAGAGAC 1341
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Db 400 AspArgValValProLeuHisGlyCysAspValAspLysLeuGlyArgCysLysLeuAsn 419
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QY 1342 GACTTCGTTGAGGTTTGTCTTTCGCTAGATCTGGTGGTAACTGGGAAGCATTTTCGCT 1401
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Db 420 AspPheValLysGlyLeuSerTrpAlaArgSerGlyGlyAsnTrpGlyGluCysPheSer 439
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RESULT 14
US-09-044-718-12
; Sequence 12, Application US/09044718
```

```
Patent No. 6391605
GENERAL INFORMATION:
APPLICANT: KOSTREWA, Dirk
APPLICANT: PASAMONTES, Luis
APPLICANT: TOMSCHY, Andrea
APPLICANT: van LOON, Adolphus
APPLICANT: VOGEL, Kurt
APPLICANT: WYSS, Markus
TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: Modified Phytases
CURRENT APPLICATION NUMBER: US/09/044,718
CURRENT FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
PRIOR FILING DATE: 1997-03-25
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 449
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-09-044-718-12

Alignment Scores:
Pred. No.: 1,08e-175 Length: 449
Score: 1878.50 Matches: 351
Percent Similarity: 87.73% Conservative: 35
Best Local Similarity: 79.77% Mismatches: 53
Query Match: 75.56% Indels: 1
Gaps: 4

US-09-488-265b-30 (1-1404) x US-09-044-718-12 (1-449)

QY 82 TCTCAGCTCTGACACTGTTGACGGTGGTACCAATGTTTCCAGAAATTCCTCAGTIS 141
DB 11 SerLysSerCysAspThrValAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeu 30
QY 142 TGGGTACATACCTCCATCTCTTCCTTCGCTGACCAATCTGCTATTTCCTCCAGAGTII 201
DB 31 TrpGlyGlnTyrSerProPhePheSerLeuGluAspGluLeuSerValSerSerLysLeu 50
QY 202 CCAAGGGTGTAGAGTACTTTCGTTCAAGTTTGTCTAGACACGGTGTGATACCCA 261
DB 51 ProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyAlaArgTyrPro 70
QY 262 ACTTCTCTCGCTCTAAGCGCTACTCTGCTTTGATTGAAGCTATTCAAAAGACGGTACT 321
DB 71 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 90
QY 322 GCTTTCAGGGTAGTAGCTTCTTTCGAGACTTACACTACACTTTGGTGGTGTGACGAC 381
DB 91 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAspAsp 110
QY 382 TTGACTCCATTCGGTGAACAACAAATGGTAACTCTGCTATTAGTTCTACAGAAGATAC 441
DB 111 LeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 130
QY 442 AAGCGTTTGGGTAGAAAGATGTTCCATTTCATTAGAGCTTCTGCTTCTGACAGAGTATT 501
DB 131 LysAlaLeuAlaArgSerValProPheIleArgAlaSerGlySerAspArgValIle 150
QY 502 CTTCTGCTGTAAGAGTTCATTGAGCTTCCAACTCTGCTGCTGCTGCTGCTGCTGCTGCT 561
DB 151 AlaSerGlyGlyLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaAspProGlyAla 170
QY 562 AACCCACACCAAGCTTCTCCAGTATTAACTGTTATTATTCAGAGAGGTGCTGTTACAC 621
DB 171 Thr-----AsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 189
QY 622 AACATTGGACCGAGGTGTTGCTGCTGCTTTCGAGAGTTCGAGAGTTCGAGAGTTCGAG 681
DB 190 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 209
QY 682 GAAGCTACTTCACTGCTGTTTTCGCTCCCACTTAGAGCTTAGATTGGAGAGCTCACTTG 741

Db 210 AlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAlaArgAlaGluLysHisLeu 229
QY 742 CCAGGTGTTAACTTGACTGACGAGACGCTGTTAACTTGATGACGACATGCTGCCATTCGAC 801
DB 230 ProGlyValThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAsp 249
QY 802 ACTGTTGCTAGAACTTCTGACGCTACTCAATGCTCTCCATTCCTGCTGCTGCTGCTGCTC 861
DB 250 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 269
QY 862 GACGAATGGAATTCATACGACTACTTCAATCTTGGGTAACTACTACGCTGCTGCTGCTGCT 921
DB 270 AsnGluTyrLysLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrGlyTyrGlyAla 289
QY 922 GGTAAACCATTTGGTCCAGCTCAAGGTGTTGGTTTACGAATGATGCTGCTGCTGCTGCT 981
DB 290 GlyAspProLeuGlyProAlaGlyIleGlyPheThrAsnGluLeuIleAlaArgLeu 309
QY 982 ACTCAGCTCTCCAGTTCAGACGACACTTCTACTACACACTTTGGACTCTTAACCCAGCT 1041
DB 310 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 329
QY 1042 ACTTCCCATTTGACGCTACTTGTACGCTGACTTCTCTCAGCAGACACTATGCTTCT 1101
DB 330 ThrPheProLeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSer 349
QY 1102 ATTTCTCTCGCTTTCGCTTGTACACGCTACTACGCTTGTCTGCTGCTGCTGCTGCTGCT 1161
DB 350 IlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgThrSerValGlu 369
QY 1162 TCTATTGAAGAACTGACGGTTCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1221
DB 370 SerAlaLysGluLeuAspGlyTyrSerAlaSerThrValValProPheGlyAlaArgAla 389
QY 1222 TACGTGTGAATGCAATGTAAGCTCAAGCTCAAGGAAACCATTTGGTGAAGTTTGGTTAAC 1281
DB 390 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 409
QY 1282 GACAGAGTTGTTCCATTCGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1341
DB 410 AspArgValValProLeuHisGlyCysAspValAspLysLeuGlyArgCysLysLeuAsn 429
QY 1342 GACTTCGTTGAAGTTTGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1401
DB 430 AspPheValLysGlyLeuSerThrPalaArgSerGlyGlyAsnTrpGlyGlyCysPheSer 449

RESULT 15
US-09-044-718-81
Sequence 81, Application US/09044718
Patent No. 6391605
GENERAL INFORMATION:
APPLICANT: KOSTREWA, Dirk
APPLICANT: PASAMONTES, Luis
APPLICANT: TOMSCHY, Andrea
APPLICANT: van LOON, Adolphus
APPLICANT: VOGEL, Kurt
APPLICANT: WYSS, Markus
TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: Modified Phytases
CURRENT APPLICATION NUMBER: US/09/044,718
CURRENT FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
PRIOR FILING DATE: 1997-03-25
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 81
LENGTH: 465
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-09-044-718-81

Alignment Scores:
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Best Local Similarity:	76.45%	Mismatches:	72
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US-09-488-265B-30 (1-1404) x US-09-044-718-81 (1-465)

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QY	61	GCCTGGGTCCTCGTGGTAACCTCTACCTCTGTGTGACACTGTTTACGGTGGTTACCAATGT	120
DB	21	AlaProSerSerAlaGly--SerLysSerCysAspThrValAspLeuGlyTyrGlnCys	39
QY	121	TTCCCAAGAAATTCCTACCTGTGGGGTACATACTCTCCATCTCTCTCTTGGCTGCAGAA	180
DB	40	SerProAlaThrSerHisLeuTyrGlyGlnTyrSerProPheSerLeuGluAspGlu	59
QY	181	TCGTGCTATTCTCCAGAGGTTCCAAAGGGTGTAGACTTACTTTCGTTCAAGTTTGTCT	240
DB	60	LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer	79
QY	241	AGACACGGTGTAGATACCAACTCTCTCGCTTAAGCGTACTCTGCTTTGATTGAA	300
DB	80	ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysLysLysLeuValThr	99
QY	301	GCTATTCAAAGACGCTACTGCTTTCAGGGTAACTACGCTTCTTGAAGACTTACAA	360
DB	100	AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysTyrAsn	119
QY	361	TACACTTTGGSGTGTGACGACTTGACCTCCATTCGGTGAACAACAATGTTAACTCTGT	420
DB	120	TyrThrLeuGlyAlaAspAspLeuThrAlaPheGlyGlnGlnLeuValAsnSerGly	139
QY	421	ATTAAGTTCTACAGAGATACAAAGGCTTGCTTGAAGAAGATTGTTCCATTAGTAGCT	480
DB	140	IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla	159
QY	481	TCGTGTTCTGACAGAGTTATTGCTTCTGCTGAAAGTTCATTGAAGGTTCCAACTGCT	540
DB	160	SerGlySerAspArgValIleAlaSerGlyGlyLysPheIleGlyPheGlnGlnAla	179
QY	541	AGTTGGCTGACCCAGGTGCTTAACCCACACACAGCTTCTCCAGTTATTACGTTATTAT	600
DB	180	LysLeuAlaAspProGlyValThr---AsnArgAlaAlaProAlaIleSerValIleIle	198
QY	601	CSAGAAGTGTCTGGTTACAAACAACACTTGCACACAGCTTGTGTACTGCTTCCGAAGA	660
DB	199	ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla	218
QY	661	TCTGAATTGGGTGACAGCGTTGAAGCTAACTTCACTGCTGCTTTCGCTCCACCAATTAG	720
DB	219	SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg	238
QY	721	GCTAGATTGGAAGCTCACTTGCAGAGGTTAACCTTGACTGACGAACAGCTGTGTAACTTG	780
DB	239	AlaArgAlaLysLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu	258
QY	781	ATGGACATGTGTCATTCGACACTGTTGCTTAGAACTTCTTGACGCTACTCAATTGTCTCA	840
DB	259	MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro	278
QY	841	TCTGTGACTTCTTCACTCAGCAGAAATGGATTCAATACGACTACTTGCATCTTTGGGT	900
DB	279	PheCysGlnLeuPheThrHisAsnGluTyrLysLysTyrAsnTyrLeuGlnSerLeuGly	298
QY	901	AGTACTACGGTTACGGTGTGGTAACCATTTGGGTCCAGCTCAAGGTGTGGTTTCGTT	960
DB	299	LysTyrTyrGlyTyrGlyValaGlyAsnProLeuGlyValProAlaGlnGlyIleGlyPheThr	318

Search completed: October 3, 2003, 08:57:32
Job time : 44.0567 secs

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Db	339	ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetIyrValAspPheSer	358
QY	1081	CACGACAAACACTATGGTTTCTATTTCITTCGGTTTGGGTTTGTACACGGTACTAAGCCA	1140
Db	359	HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro	378
QY	1141	TTGTCTACTACTCTGTTGAATCTATTGAAGAACTGACGGTTACTCTGCTCTCTGCACT	1200
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QY	1201	GTTCCATCTCGCTGTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAGGAACCA	1260
Db	399	ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro	418
QY	1261	TTGGTTAGAGTTTGGGTTTACGACAGAGTGTTCATTCACGGTGTGCGTGTGACAAAG	1320
Db	419	LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys	438
QY	1321	TTGGGTAGATCTAGAGAGAGCACTCGTGTGAAGGTTTGTCTTTCGCTAGATCTGCTGGT	1380
Db	439	LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyCly	458
QY	1381	AACTGGGAGAAATGTTTCGCT	1401
Db	459	AsnTrpGlyGluCysPheSer	465

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 3, 2003, 08:05:37 ; Search time 70.6311 Seconds
(without alignments)
6289.894 Million cell updates/sec:

Title: US-09-488-265b-28

Perfect score: 2480

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Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 1175308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM-ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09488265 -ACCN_1_1_278 -runat_03102003_074815_12295
-NCPUP=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FCAPOP=6 -FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description

ALIGNMENTS

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US-10-083-452-9
: Sequence 9, Application US/10083452
: Publication No. US20020127218A1
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: TITLE OF INVENTION: Phytase Variants
: FILE REFERENCE: 5618 500-US
: CURRENT APPLICATION NUMBER: US/10/083,452
: CURRENT FILING DATE: 2002-02-26
: PRIOR APPLICATION NUMBER: US/09/273,871
: PRIOR FILING DATE: 1999-03-22
: PRIOR APPLICATION NUMBER: PA 1998 00407
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: PA 1998 00806
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: PA 1998 01176
: PRIOR FILING DATE: 1998-09-18
: PRIOR APPLICATION NUMBER: PA 1999 00091
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/080,129
: PRIOR FILING DATE: 1998-03-31
: PRIOR APPLICATION NUMBER: 60/090,675
: PRIOR FILING DATE: 1998-06-25

Sequence 9, Appli
Sequence 32, Appli
Sequence 5, Appli
Sequence 8, Appli
Sequence 78, Appli
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Sequence 11, Appli
Sequence 24, Appli
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Sequence 4, Appli
Sequence 16, Appli
Sequence 21, Appli

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NUMBER OF SEQ ID NOS: 15
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; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-10-083-452-9

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Best Local Similarity: 97.86% Mismatches: 7
Query Match: 97.10% Indels: 0
DB: 14 Gaps: 0

US-09-488-265B-28 (1-1404) x US-10-083-452-9 (1-467)

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DB 41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60
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QY 541 AGCTTGGTGCACCGAGTTCACACCAACCAAGCTTCTCAGTTATTACGTGATCATT 600
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DB 201 ProGluGlySerGlyTyrAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220
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DB 221 SerGluLeuGlyAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
QY 721 GCTAGATTGGAAGCTACTTCCAGGCTTACTTGTGCTGACGAGACGCTGTTTACTTG 780
DB 241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260
QY 781 ATGGACATGTGTCCTTCCGACACTGTCGCTAGACTTCTGACGCTACTGAATGCTCTCCA 840
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DB 281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly 300
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RESULT 2

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; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selten
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002

CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/233,510
 FILING DATE: 20-JAN-1999
 APPLICATION NUMBER: 07/688,578
 FILING DATE: 24-MAY-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Murashige, Kate H.
 REGISTRATION NUMBER: 29,954
 REFERENCE/DOCKET NUMBER: 24615-20026.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-327-7250
 TELEFAX: 415-327-2951
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 467 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-10-079-709-32

Alignment Scores:

Pred. No.: 1,84e-152 Length: 467
 Score: 1875.00 Matches: 353
 Percent Similarity: 84.37% Conservative: 43
 Best Local Similarity: 75.59% Mismatches: 73
 Query Match: 75.60% Indels: 0
 DB: 15 Gaps: 0

US-09-488-265b-28 (1-1404) x US-10-079-709-32 (1-467)

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QY 1 ATGGCGGTTCGTCGCTACTGTGGGTACCTGCCACCTTGTCGCTCCACATCCGCTACC 60
DB 1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuSerGlyValThrSerGlyLeu 20
QY 61 GCCTTGGGTCCGCGGGTAATTCACCTCTTGTGACACTGTGACGGTGTACCAATGT 120
DB 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40
QY 121 TTCCCAGAAATTCACATGTGGGTACCTACTCTCCACTTCTCTTGGGACAGCAA 180
DB 41 PheSerGluThrSerHisLeuTyrGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60
QY 181 TCCTGCTATTCCTCCAGACGCTCCACACGACTGTAGACTTCTTCGTCAGATTTCGT 240
DB 61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80
QY 241 ACACAGGTGTAGATACCAACTCTCTTCGCGCTAAGGCTTACTCTGCTTGAATCAA 300
DB 81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
QY 301 GCTATTCAAAGACGCTACTCTCTTCAAGGTGAAGTACGCTTCTTGAAGACTTACAAC 360
DB 101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 361 TACACTTGGGTGCTGACGACTTGACTCCATTCGCTGGTGAACCAACCAAGTTCCTGGT 420
DB 121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 421 ATTAGCTTCTACAGAGATACAGGCTTGGCTAGAAAGATGTTCATTCATTAAGACT 480
DB 141 IleLysPheTyrGlnArgTyrGlnSerLeuThrArgAsnIleValProPheIleArgSer 160
QY 481 TCTGGTCTCAGACAGTTATTCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180
QY 541 AAGTTGGCTGACCCAGGTTCCTCAACACACCAACGCTTCTCCAGTTATTAAGCTGATCAT 600
DB 181 LysLeuLysProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200
QY 601 CCAGAGGATCCGGTTACAAACAACTTTGGACACGCTACTGTACTGCTTCCGACAG 660
DB 601 LysLeuLysProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200

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DB 201 SerGluAlaSerSerSerAsnThrLeuAspProGlyThrCystThrValPheGluAsp 220
QY 661 TCTGAATAGGTGACGAGCTTGAAGCTTAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 221 SerGluLeuAlaAspThrValGluAlaAsnPheIleAlaThrPheValProSerIleArg 240
QY 721 GCTAGATTGGAAGCTGACTTGCAGGCTTACTTGTAGCTGACGAGAGAGGTTGTTACTTG 780
DB 241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260
QY 781 ATGGACATGTGTCATTCGACACTGTCGCTAGACACTTCTGACGCTACTGATTCGCTCA 840
DB 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
QY 841 TCTGTGCTTGTTCCTCCTCAGCAGATGGAATCCAAATACGACTACTTGCACCAAGCTTGGT 900
DB 281 PheCysAspLeuPheThrHisAspGlnTrpIleAsnIleAspTyrLeuGlnSerLeuLys 300
QY 901 AAGTACTAGGTTACGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
DB 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
QY 961 AACGAATGATTGCTAGATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020
DB 321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340
QY 1021 ACTTTGGACTCTAACCCAGCTACTTCCCAATGAAGCTACTTTGTGACGCTGACTTCTCT 1080
DB 341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360
QY 1081 CAGCAACACTATGATATCTATTTCTTCGCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 1140
DB 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrIlePro 380
QY 1141 TTGCTTACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1200
DB 381 LeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyrIle 400
QY 1201 GTTCCATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnPro 420
QY 1261 TTGGTTAGAGTTTGGTTAACGACAGAGTTGTTTCCATTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440
QY 1321 TTGGGTAGATGTAAAGAGACGACTTCTGTTGAGGTTTGTCTTTCGCTAGATCTGCTGCT 1380
DB 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGCTCAATGTTTCGCT 1401
DB 461 AspTyrAlaGluCysPheAla 467

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RESULT 3

US-10-229-358-5
 Sequence 5, Application US/10229358
 Publication No. US20030124700A1
 GENERAL INFORMATION:
 APPLICANT: Stafford, Christian F.
 APPLICANT: Trinci, Anthony P.J.
 APPLICANT: Brookman, Jayne L.
 TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
 TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating San
 FILE REFERENCE: GC596-2
 CURRENT APPLICATION NUMBER: US/10/229,358
 CURRENT FILING DATE: 2002-08-26
 PRIOR APPLICATION NUMBER: US 60/148,960
 PRIOR FILING DATE: 1999-08-13
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 5
 LENGTH: 467

TYPE: PRT

ORGANISM: Aspergillus niger

US-10-229-358-5

Alignment Scores:

Pred. No.: 1.84e-152 Length: 467
Score: 1875.00 Matches: 353
Percent Similarity: 84.37% Conservativity: 41
Best Local Similarity: 75.59% Mismatches: 73
Query Match: 75.60% Indels: 0
DB: 15 Gaps: 0

US-09-488-265b-28 (1-1404) x US-10-229-358-5 (1-467)

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Qy 1 ATGGCGTGTTCGTCGGTACTGTCACATGCCACCTTGTCGGTTCACATCCGGTAC 50
Db 1 MetGlyValSerAlaValLeuProLeuLeuSerGlyValThrSerGlyLeu 20
Qy 61 GCCTTGGTCTCGTGTGTAATTCACCTCTCTGCACACTGCTTCACCGTGCITACCAATCT 120
Db 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyThrGlnCys 40
Qy 121 TTCACAGAAATTCCTACTCTCTGCGGTACCTACTCTCCACTCTCTTTGGCAGACGAA 180
Db 41 PheSerGluThrSerHisLeuTyrGlyGlnThrAlaProPheSerLeuAlaAsnGlu 60
Qy 181 TCTGCTATTCTCCAGAGCTCCAGACGACTGTAGAGTACTTCTCCAGTTTGTCT 240
Db 51 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80
Qy 241 AGACACGGTGTAGATACCCCACTCTCTGCGTCTAAGCCTTACTCTGCTTTGATGAA 300
Db 81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuLeuGlu 100
Qy 301 GCTATTCAAAGACGCTACTGCTTTCACGGTAACTACGCTTCTTGAAGACITACAC 360
Db 101 GluIleGlnGlnAsnAlaThrPheAspGlyLysTyrAlaPheLeuLysThrThrAsn 120
Qy 361 TACACTTGGTGTGTCGACTTACCTCCATTCGGTGAACCAACCAATGGTTAACTCTGT 420
Db 121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
Qy 421 ATTAAGTCTCAGACAGATACAGGCTTTGGCTAGAAGATTTGTCATTCATTAAGCT 480
Db 141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160
Qy 481 TCTGCTTCTGACAGAGTATTGCTTCTGCTGAAAAGTTTCATTAAGGCTTTCCCAATCTGT 540
Db 161 SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 180
Qy 541 AAGTTGGTGCACAGGCTTCACACACACACAGCTTCTCCAGTTATTACGTGATCAT 600
Db 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValIle 200
Qy 601 CCAGAGGATCCGGTTACAAACACACTTGGACACCGTACTTGTACTGCTTTCGAGAC 660
Db 201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
Qy 661 TCTGAATTAGTGACGAGCTTGAAGCTTAACCTTCACTGCTTGTGCTCCAGCTATTAGA 720
Db 221 SerGluLeuAlaAspThrValIleAlaAsnPheThrAlaThrPheValProSerIleArg 240
Qy 721 GCTAGATTGGAGCTGCTCCAGGCTTACTTGTACTGACGACGAGCTGTTTACTTG 780
Db 241 GlnArgLeuGlnAsnAspSerGlyValThrLeuThrAspThrGluValThrThrLeu 260
Qy 781 ATGGACATGTGTCATTCACACTGTCGCTAGAACITTCGACGCTACTGAATTCCTCCA 840
Db 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
Qy 841 TTCTGCTGCTTGTTCACCTCAGCAGAGATGGATCCAACTACTTCCAAAGCTTGGGT 900
Db 281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300

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Qy 901 AAGTACTACGTTTACGGTCTGTGTAACCCACTGGGTCCAGCTCAAGGTCTTGGTTCCGT 960
Db 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
Qy 961 AAGCAATGATTCCTAGTAGTACTCTCTCCAGTTTCAAGACACCACTTCTACTAACCA 1020
Db 321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340
Qy 1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATCTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db 341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360
Qy 1081 CAGCAACAACTATGATATCTATTCTTCGCTTTCGGTTTGTATACAAAGGTACCAAGCCA 1140
Db 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380
Qy 1141 TGTCTACTACTCTCTGTTGAATCTATTGAAGAACTACGGTTACTCTCTCTTCTGGACT 1200
Db 381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaThrThr 400
Qy 1201 GTTCATTCGCTGCTAGAGCTTACGTGTGAATGATGCAATGTCAGCTGAAAGGAACCA 1260
Db 401 ValProPheAlaSerArgLeuTyrValGluMetGlnCysGlnAlaGluGlnGluPro 420
Qy 1261 TGTGTTAGAGTTTGGTTAACGACAGAGTTGTTCATTCACGGTGTGCTGTGACAAAG 1320
Db 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440
Qy 1321 TTGGGTAGATGTAGAGACAGACCTTCGTTGAAGGTTTGTCTTTCCTAGATCTGGTGT 1380
Db 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
Qy 1381 AACTGGGCTCAATCTTTCGCT 1401
Db 461 AspTrpAlaGluCysPheAla 467

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RESULT 4

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US-10-083-452-8
; Sequence 8, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083.452
; PRIOR FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273.871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/050,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-083-452-8

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Alignment Scores: 8.97e-152 Length: 465
Pred. No.: 1867.00 Matches: 355
Score: 83.73% Conservativity: 36


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QY 361 TACACITTTGGTGTGCTACGACTTGTACCTCCATTCGGTGAAACCAAAAGGTTAACTCTGGT 420
Db 120 TyrThrLeu:GlyAlaAspSerLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAAGTTCTACAGAAGATTAAGGCTTTGGCTAGAAAGATTTCTCCATTCATTAAGCT 480
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 481 TCTGGTCTCAGACAGATTATGCTTCTGCTGCAAAAGTTCATTGAAGTTTCCAACTCTGT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlnGlnAla 179
QY 541 AAGTTGCTCAGCCAGGTTCTCAACCAACCAAGCTTCTCAGCTTATTAACGTGATCAIT 600
Db 180 LysLeuAlaAspProGlyAla---ThrAsnArgAlaAlaProAlaIleSerValIleIle 198
QY 601 CCAGAAGATCCGGTTACAAACACACTTTGGACACAGGTACTTGTACTGCTTCTCGAAGAC 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATTAGGTGACGAGCTGAAGCTTAAGTTCACCTGCTTGTTCGCTCCAGCTATTAGA 720
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATTGGAAGCTGACTTGCACAGGTGTACTTTGACTGACGAAGACGTTGTACTTIG 780
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGGACATGTGTCATTGACACATGTGCTAGAACCTTCTGACGCTACTGAATTTGTCTCCA 840
Db 259 MetAspMetCysSerPheAspPheThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TTCGTGCTTGTTCACCTCAGCAGGATGATGATCCAAATACGACTACTTCGAAAACCTTGGT 900
Db 279 PheCysGlnLeuPheThrHisAsnGluThrLysLysTyrAsnTyrLeuGlnSerLeuGly 298
QY 901 AAGTACTACGGTTACGGTGTGCTGCTAAACCATTTGGGTCACGCTCAAGGIGTGTGCTCG 960
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 961 AACGAATTGATTGCTAGATTGACTCCTCTCCAGTTCACACACACACTTCTACTACCAAC 1020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGACCTCTACCCAGCTACTTCTCCATTGACCGCTACTTGTACGCTGACTTCTCT 1080
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1081 CACGACAACTATGATATCTATTTCTTCGCTTTGGGTTGTACACGCTACCAAGCCA 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
QY 1141 TTGCTACTACTCTGTTGAATCTATTGAAGAACTACCGGTTACTTGTCTTGGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
QY 1201 GTTCCATTGCTGCTAGAGCTTACGTTGAATGATCAATGTCAAGCTGAAAAGGAACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSorGluLysGluPro 418
QY 1261 TTGTTTAGAGTTTGGTTAAACGACAGAGTTGTTCCATTGACCGGTTGTGTTGTGACAG 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY 1321 TGGGTAGATCTAGACAGACGACTTCTGTTCAAGGTTTGTCTTCGCTAGATCTGGTGGT 1380
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
QY 1381 AACTGGGCTGAATGTTTCGCT 1401
Db 459 AsnTrpGlyGluCysPheSer 465
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RESULT 7

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US-10-083-452-11
: Sequence 11, Application US/10083452
: Publication No. US20020127218A1
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: TITLE OF INVENTION: Phytase Variants
: FILE REFERENCE: 5618.500-US
: CURRENT APPLICATION NUMBER: US/10/083,452
: PRIOR FILING DATE: 2002-02-26
: PRIOR APPLICATION NUMBER: US/09/273,871
: PRIOR FILING DATE: 1999-03-22
: PRIOR APPLICATION NUMBER: PA 1998 00407
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: PA 1998 00806
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: PA 1998 01176
: PRIOR FILING DATE: 1998-09-18
: PRIOR APPLICATION NUMBER: PA 1999 00091
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/080,129
: PRIOR FILING DATE: 1998-03-31
: PRIOR APPLICATION NUMBER: 60/090,675
: PRIOR FILING DATE: 1998-06-25
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 11
: LENGTH: 467
: TYPE: PRT
: ORGANISM: Aspergillus ficuum
US-10-083-452-11
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Alignment Scores:
Pred. No.: 1,98e-151 Length: 467
Score: 1863.00 Matches: 351
Percent Similarity: 83.94% Conservative: 41
Best Local Similarity: 75.11% Mismatches: 75
Query Match: 75.12% Indels: 0
DB: 14 Gaps: 0

US-09-488-265b-28 (1-1404) x US-10-083-452-11 (1-467)
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QY 1 ATGGGGGCTGTCGTGCTGCTACTGCTCCATTTGCACACCTTGTTCGGTTCCACATCCGGTACC 60
Db 1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20
QY 61 GCCTTGGGCTCCTCGTGGTAATTCTCCTCTGTGACACTGTTGACGGTGGTTACCAATGT 120
Db 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40
QY 121 TTCCCAAGAAATTTCTCCTGTTGGGTACTACTCTCCATACCTTCTCTTGGCAGACGAA 180
Db 41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60
QY 181 TGTGCTATTCTCCAGACGCTTCCAGACGACTGTAGAGTACTTTCGTTCAAGTTTGTCT 240
Db 61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80
QY 241 AGACACGGTGTAGATACCACTTCTCTGGCTGTAAAGCTTACTGCTGCTTGTGATTCAA 300
Db 81 ArgHisGlyValArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
QY 301 GTATTTCAAAAGAAAGCTACTGCTTCAAGGTAAAGTACGCTTCTTGAAGACTTACAAC 360
Db 101 GluIleGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 361 TACACTTTGGTGTGACGACTTGACTCCTCATTCCGTTGAAACCAAAAGTAACTCTGGT 420
Db 121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 421 ATTAAGTTCTACAGAGATACAAAGCTTTGGCTAGAAAGATTTGCTCATTTAGACT 480
Db 141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 3, 2003, 07:48:21 ; Search time 21.0567 Seconds
(without alignments)
5642.336 Million cell updates/sec

Title: US-09-488-265B-30
Perfect score: 2486
Sequence: 1 atggggctgttcgtcgtct.....gggaagaatttcgcttaa 1434

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310858 residues
Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODEL=frame-n2p.model -DEV=xlp
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-DB=Issued_Patents_AA -QFMI=fastan -SUFFIX=oct3.rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09488265.ecgn.1.1.99 -runat_03102003_074813_12239 -NCPU=6 -ICPU=3
-NO_MMAPP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
Issued_Patents_AA:*
1: /cgn2.6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2.6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2.6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2.6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2.6/ptodata/1/iaa/PCBUS.COMB.pep.*
6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2308	92.8	467	4	US-09-273-871A-9
2	2182	87.8	441	3	US-09-121-425-1
3	2182	87.8	441	3	US-09-634-493A-1
4	2170	87.3	467	3	US-09-121-425-2
5	2170	87.3	467	4	US-09-634-493A-2
6	1888	75.9	465	3	US-08-868-435-33
7	1888	75.9	465	4	US-08-744-231-33
8	1888	75.9	465	4	US-09-044-718-78
9	1888	75.9	465	4	US-09-636-499-6
10	1888	75.9	465	4	US-09-273-871A-8
11	1860	75.6	465	4	US-09-044-718-80
12	1879	75.6	465	4	US-09-044-718-79
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					Sequence 1, Appl
					Sequence 2, Appl
					Sequence 3, Appl
					Sequence 4, Appl
					Sequence 5, Appl
					Sequence 6, Appl
					Sequence 7, Appl
					Sequence 8, Appl
					Sequence 9, Appl
					Sequence 10, Appl
					Sequence 11, Appl
					Sequence 12, Appl
					Sequence 13, Appl
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					Sequence 97, Appl
					Sequence 98, Appl
					Sequence 99, Appl
					Sequence 100, Appl

Alignment Scores:
Pred. No.: 7.66e-218
Score: 2309.00
Percent Similarity: 95.72%
Length: 467
Matches: 436
Conservative: 11

ALIGNMENTS

RESULT 1

US-09-273-871A-9

Sequence 9, Application US/09273871A

Patent No. 6514495

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan;

TITLE OF INVENTION: Phytase Variants

FILE REFERENCE: 5618 500-US

CURRENT APPLICATION NUMBER: US/09/273.871A

CURRENT FILING DATE: 1999-03-22

PRIOR APPLICATION NUMBER: PA 1998 00407

PRIOR FILING DATE: 1998-03-23

PRIOR APPLICATION NUMBER: PA 1998 00806

PRIOR FILING DATE: 1998-06-19

PRIOR APPLICATION NUMBER: PA 1998 01176

PRIOR FILING DATE: 1998-09-18

PRIOR APPLICATION NUMBER: PA 1999 00091

PRIOR FILING DATE: 1999-01-22

PRIOR APPLICATION NUMBER: 60/080.129

PRIOR FILING DATE: 1998-03-31

PRIOR APPLICATION NUMBER: 60/090.675

PRIOR FILING DATE: 1998-06-25

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

LENGTH: 467

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Variation

US-09-273-871A-9

Sequence 3, Appl
Sequence 12, Appl
Sequence 81, Appl
Sequence 82, Appl
Sequence 8, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 32, Appl
Sequence 20, Appl
Sequence 2, Appl
Sequence 12, Appl
Sequence 3, Appl
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Sequence 3, Appl
Sequence 5, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 35, Appl
Sequence 35, Appl
Sequence 12, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 2, Appl
Sequence 2, Appl

Best Local Similarity: 93.36% Mismatches: 20
Query Match: 92.84% Indels: 0
DB: 4 Gaps: 0

US-09-488-265B-30 (1-1404) x US-09-273-871A-9 (1-467)

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QY 61 GCGTGGGCTCTGGTAACTCTCACTCTTGTGACACTGTGTGAGGGGTGATACCAATGT 120
DB 21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyGlyCys 40
QY 121 TTCGAGAAATTCCTCACTTGGGGTACATACCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
DB 41 PheProGluIleSerHisLeuIleProGlyGlnThrSerProTyrPheSerLeuGluAspGlu 60
QY 181 TCTGCTATTCTCCAGACGTTCCAAAGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
DB 61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80
QY 241 AGACAGGCTGTAGATACCAACTCTCTCTGGCTCTAAGGGCTACTCTGCTTGTGATTGAA 300
DB 81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGlu 100
QY 301 GCTATTCAAAGAAGCTACTCTCTCTCAAGGTAAGTACGCTTCTTGAAGACTTTACAA 360
DB 101 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 361 TACACTTGGGTGCTGACAGCTTACTCCATTCGTTGAGAACAAAGTTAACTCTGGT 420
DB 121 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 140
QY 421 ATTAAGTCTACAGAGATACAAAGCTTGGCTAGAGAGATTTCCATTCATITAGACT 480
DB 141 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 160
QY 481 TCTGGTTCTGACAGAGTTATTCTCTCTGCTGAAAGTTTCATTGAAGGTTTCCAACTGCT 540
DB 161 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 180
QY 541 AAGTTGGCTGACCCAGGCTCTAACCCACACCAAGCTTCTCCAGTTATTAACGTTATTAT 600
DB 181 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspValIleIle 200
QY 601 CCAGAGGCTGCTGTACACACACTTTGGACCCAGGTTTGTGCTACTCTTCCAGAA 660
DB 201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220
QY 661 TCTGAATTGGGTGACGACGCTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
DB 221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
QY 721 GCTAGATTGGAGCTCCTTGCAGGTTGTACTTGAAGCTGACGAGAGAGCTTGTACTTG 780
DB 241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260
QY 781 ATGGACATGTGCTTCCATTCGACACTGTGTAGAACTTCTGACGCTACTCAATTTCTCCA 840
DB 261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280
QY 841 TCTGTGACTTGTCTACTCAGCAGCAATGATTCAAATACGACTTCTTGAATCTTTTGGT 900
DB 281 PheCysAlaLeuPheThrHisAspGluTyrArgGlnTyrAspTyrLeuGlnSerLeuGly 300
QY 901 AAGTACTACGGTTACGGTCTGCTACCCATTTGGGTCCAGCTCAAGGTTGTGTTTCTGTT 960
DB 301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320
QY 961 AAGCAATTGATCTAGATTGACTCTCTCCAGTTTCAAGCTTCAAGCTTCTACTACCAAC 1020
DB 321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340
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QY 1081 CAGCACAACTACTGCTTTCTATTTCCTTTCGCTTTGGTTTGTACACGGTACTTAAGCCA 1140
DB 361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380
QY 1141 TTGCTTACTACTTCTGTTGAATCTATTAAGAAGCTGACGGTTACTCTGCTTCTTGACT 1200
DB 381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTyrThr 400
QY 1201 GTTCATTCCTGCTAGAGCTTACGTTGAATGATTCATTCGCTTGAAGCTGAAAGGAACCA 1260
DB 401 ValProPheGlyAlaArgAlaTyrValGluMetGlnCysGlnAlaGluLysGluPro 420
QY 1261 TTGTTAGACTTTTGTAAACGACAGAGTTTTCCTTTCACATTCGACGGTGTGTGACAG 1320
DB 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440
QY 1321 TTGGGTAGATGTAAGACAGAGAGCTTCTGTTGAAGGTTTGTCTTTCGCTAGATCTGTT 1380
DB 441 LeuGlyArgCysLysArgAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGCAAGAATGTTTCGCT 1401
DB 461 AsnTrpAlaGluCysPheAla 467

RESULT 2
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121.425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112668.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-121-425-1

Alignment Scores:
Pred. No.: 1,73e-205 Length: 441
Score: 2182.00 Matches: 410
Percent Similarity: 95.46% Conservative: 11
Best Local Similarity: 92.97% Mismatches: 20
Query Match: 87.77% Indels: 0
DB: 3 Gaps: 0

US-09-488-265B-30 (1-1404) x US-09-121-425-1 (1-441)

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QY 139 TTGTTGGGTACATCTCTCCATTCCTTCTTGGCTACCAATCTGCTATTCTTCTCAGAC 198
DB 21 LeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAsp 40
QY 199 GTTCCAAAGGGTCTAGAGTTACTTCTGTTCAAGTTTGTCTAGACACGGTGTAGATAC 258
DB 41 ValProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyAlaArgTyr 60
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QY	259	CCAACTCTCTCGCTCAAGCGGTACTCTGCTTGAAGCTATTCAAAAGACGGCT	318
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QY	319	ACTGCTTTCAAGGTAAGTACGCTTCTTGAACACTTACAACCTACACTTTGGGTGCTGAC	378
Db	81	ThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp	100
QY	379	GACTTGACTCCATTCGGTGAACACAAATGGTTAACTCTGGTATTAAAGTTCTACAGACA	438
Db	101	AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPheTyrArgAla	120
QY	439	TACAAGCCTTGGCTAGAAAGATTGTCCTATTAGAGCTTCTGGTCTGACAGATT	498
Db	121	TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal	140
QY	499	ATTGCTTCTGCTGAAAGTTCATTGAAGGTTTCCAAATCTGCTAAGTTGGTGACCCAGGT	558
Db	141	IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProGly	160
QY	559	GCTAACCCACACAAGCTTCTCCAGTTATTAAAGTTATTATCCAGAAGTGCTGCTTAC	618
Db	161	SerGlnProHisGlnAlaSerProValIleAspValIleIleProGluGlySerGlyTyr	180
QY	619	AACAACACTTTGACACCGCTTCTGCTACTGCTTTCGAGAAATCTCAATTTGGGTGACGAC	678
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QY	679	GTTGAAGCTAACTTCACTGCTGTTTCGCTCCACCAATTAGAGCTAGATTGGAAGCTCAC	738
Db	201	ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp	220
QY	739	TTGCCAGGTGTTAACTTACTGACGACGAGCGTTGTTAACTTGATGACATGTCCTCATTC	798
Db	221	LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe	240
QY	799	GACACTGTTCTAGACITCTGACGGTACTCAATTTGCTCCTCATCTCTGACTTGTTCACT	858
Db	241	GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr	260
QY	859	CACGACGAATGGATTCAATACGACTACTTGCCTCAATCTTGGTAAAGTACTACGGTTAGGCT	918
Db	261	HisAspGluTrpArgGlnTyrAspTyrLeuInSerLeuGlyLysTyrTyrGlyTyrGly	280
QY	919	GCTGGTAACCCATTGGTCCACCTCAAGCTGTTGGTTTCCGTTAACGAATGATTGCTAGA	978
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QY	979	TTGACTCACCTCCAGTTCGAAGACCACACTTCTACTAACCCACACTTTGGACTCTAACCCCA	1038
Db	301	LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnPro	320
QY	1039	GCTACTTCCATTGAACGCTACTTTGTACGCTGACTTCTCTCACGACACACTATGGTT	1098
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QY	1099	TCTATTCTTCGCTTGGGTTGTACACGGTACTAAAGCCATTGCTACTACTTCTGTT	1158
Db	341	SerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaProLeuSerThrThrSerVal	360
QY	1159	GAATCTATTCAAGAACTGACGGTTACTCTGCTTCTTGGACTCTTCCATTGCTGCTAGA	1218
Db	361	GluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg	380
QY	1219	GCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGGAACCATTTGGTTAGAGTTTGGIT	1278
Db	381	AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal	400
QY	1279	AAGCACAGATTTGTTCCATTGCGCGGTTGTGGTGTGACAAAGTTGGGTAGATGTAGAGA	1338
Db	401	AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArg	420
QY	1339	GACACTTCGTTGAAGGTTGCTTTCGTAGATCTGGTGAAGTAACTGGAGAAATTTTC	1398
Db	421	AspAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnTrpAlaGluCysPhe	440
QY	1399	GCT 1401	
Db	441	Ala 441	
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US-09-634-493A-1			
: Sequence 1, Application US/09634493A			
: Patent No. 6579975			
: GENERAL INFORMATION:			
: APPLICANT: Lehmann, Martin			
: TITLE OF INVENTION: Consensus Phytases			
: FILE REFERENCE: consensus Phytases 13239			
: CURRENT APPLICATION NUMBER: US/09/634,493A			
: CURRENT FILING DATE: 2000-08-08			
: PRIOR APPLICATION NUMBER: US/09/121,425			
: PRIOR FILING DATE: 1998-07-23			
: PRIOR APPLICATION NUMBER: EPO 97112688.3			
: PRIOR FILING DATE: 1997-07-24			
: NUMBER OF SEQ ID NOS: 20			
: SOFTWARE: PatentIn Ver. 2.0			
: SEQ ID NO. 1			
: LENGTH: 441			
: TYPE: PRT			
: ORGANISM: Artificial Sequence			
: FEATURE:			
: OTHER INFORMATION: Description of Artificial Sequence: consensus			
: OTHER INFORMATION: sequence			
US-09-634-493A-1			
Alignment Scores:			
Pred. No.:	1,73e-205	Length:	441
Score:	2182.00	Matches:	410
Percent Similarity:	95.46%	Conservative:	11
Best Local Similarity:	92.97%	Mismatches:	20
Query Match:	87.77%	Indels:	0
DB:	4	Gaps:	0
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QY	139	TTGTGGGGTACATCTCTCCATCTCTTCTCTTGGGTGACGAATCTGCTATTTCTCAGAC	198
Db	21	LeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGluSerAlaIleSerProAsp	40
QY	199	GTTCCAAAGGGTGTAGAGTTACTTTCGTTCAAGTTTGTCTAGACACGGTGCAGATAC	258
Db	41	ValProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyAlaArgTyr	60
QY	259	CCAACTCTTCTCGGCTCAAGCGTACTCTGCTTTGATGAAGCTATTCAAAGAACGCT	318
Db	61	ProThrSerSerLysSerCysAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAla	80
QY	319	ACTGCTTTTCAAGGGTAAGTACGCTTCTTTGAAGACTTACAACCTACACTTTGGGTGCTGAC	378
Db	81	ThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp	100
QY	379	GACTTGACTCCATTCGGTGAACACAAATGGTTAACTCTGGTATTAAAGTTCTACAGACA	438
Db	101	AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPheTyrArgArg	120
QY	439	TACAAGCCTTGGCTAGAAAGATTGTTCCATTATTAGAGCTTCTGGTCTCAGAGATT	498
Db	121	TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal	140
QY	499	ATTGCTTCTGCTGAAAGTTCATTGAAGGTTTCCAAATCTGCTAAGTTGGCTGACCCAGGT	558

Db 141 lleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAlaSerProGly 160
QY 559 GCTAACCCACACCAAGCTCTCCAGTTATTAACGTTATTATTCACAGAGGTGCTGCTAC 618
Db 161 SerGlnProHisGlnAlaSerProValIleAspValIlePheProGluGlySerGlyTyr 180
QY 619 AACCAACTITGGACACCGGTTGTGCTACTGCTTCGAAGAATCTGAATCGGTGACGAC 678
Db 181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200
QY 679 GTTGAAGCTAACTTCACCTGCTGTTTCGCTCCACCAATTAGAGCTAGATTGCAAGCTCAC 738
Db 201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp 220
QY 739 TCCAGAGGTGTTAACTTCACTGACGACGACGCTGTTAACTTCATGAGGACATGTCCTATTC 798
Db 221 LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe 240
QY 799 GACACTGTTGCTAGAACTTCTGACGCTACTCAATGTCTCCATTCTGCTGCTGCTACT 858
Db 241 GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr 260
QY 859 CACGACGAATGATTCATACGACTACTTGCAATCTTTGGGTAACTAGTACGTTACGGT 918
Db 261 HisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGly 280
QY 919 GCTGTAACCCATTGGGTCCAGCTCAAGTGTGTTGTTTCGTTAAGCAATTCATTCCTAGA 978
Db 281 AlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAlaAsnGluLeuIleAlaArg 300
QY 979 TTGACTCACTCTCCAGTTCAGACACACTTCTTACTAACCCACTTTGGACTCTAACCCA 1038
Db 301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnPro 320
QY 1039 GCTACTTTCCCATTCAGAGCTACTTGTACGCTGACTTCTCTCAGCACAACACTATGCTT 1098
Db 321 AlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnSerMetile 340
QY 1099 TCTATTCTTTCGCTTGGGTTGTGACACGGTACTAAGCCATTGCTACTACTTCIGTT 1158
Db 341 SerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaProLeuSerThrThrSerVal 360
QY 1159 GAATCTATTGAAGAAGCTGACGGTTPACTCTGCTTCTGAGCTGTTCCATTCCGCTGCTAGA 1218
Db 361 GluSerIleGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg 380
QY 1219 GCTTACGCTGAATGCTCAATGCTCAAGCTGAAAGGACCACTGCTTAGAGTTTGGTT 1278
Db 381 AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400
QY 1279 AACGACAGAGTGTTCCTCATTTGACGCTGTTGTGTTGACAGTTGGGTAGATGIAACAGA 1338
Db 401 AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArg 420
QY 1339 GAGGACTTCGTTGAGGTTTGTCTTCGCTAGATCTGTTGGTAACTGGGAGAGATGTTTC 1398
Db 421 AspAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnTrpAlaGluCysPhe 440
QY 1399 GCT 1401
Db 441 Ala 441

RESULT 4

US-09-121-425-2
: Sequence 2, Application US/09121425
: Patent No. 6153418
: GENERAL INFORMATION:
: APPLICANT: Lehmann, Martin
: TITLE OF INVENTION: Consensus Phytases
: FILE REFERENCE: Consensus phytases 13239
: CURRENT APPLICATION NUMBER: US/09/121.425
: CURRENT FILING DATE: 1998-07-23
: EARLIER APPLICATION NUMBER: EPO 97112688.3.

: EARLIER FILING DATE: 1997-07-24
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 2
: LENGTH: 467
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: consensus
: OTHER INFORMATION: sequence
: US-09-121-425-2

Alignment Scores:
Pred. No.: 2,696-204 Length: 467
Score: 2170.00 Matches: 416
Percent Similarity: 87.68% Conservative: 11
Best Local Similarity: 85.42% Mismatches: 20
Query Match: 87.29% Indels: 40
Gaps: 2

US-09-488-265B-30 (1-1404) x US-09-121-425-2 (1-467)

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Db 21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40
QY 121 TCCCCAGAAATTTCTACITTSIGGGTATACATCTCCATCTCTCTCTCTCTCTCTCTCT 180
Db 41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60
QY 181 TCTGCTATTTCTCAGACGTTCCAAAGGGTGTAGAGTTACTTCTGCTCAAGTTTGTCT 240
Db 61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80
QY 241 AGACACGGTCTAGATACCCAACTTCTCTCGCTCTAAGCGGTACTCTGCTTGTATTGAA 300
Db 81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla----- 97
QY 301 GCTATTCAAAAGAACGCTACTGCTTTCAAGGGTAACCTGCTTCTTGTGAAGACTTACAAC 360
Db 98 -----ThyTrpAsn 100
QY 361 TACACTTTGGGTGCTGACGACTTGACTTCCTCCATTCGGTCAACAACAATGCTTAACTCTGT 420
Db 101 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120
QY 421 ATTAAGTTCTACAGAAGATACAGGCTTTGGCTAGAAAGATTGTCATTCATTATTAGACT 480
Db 121 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleAlaGla 140
QY 481 TCTGGTTCTGACAGAGTTATGCTTCTGCTGAAAGTTTCATTGAAGTTTCCAACTGCT 540
Db 141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160
QY 541 AAGTTGGTCAACCGAGTGTAAACCCACCAAGCTTCTCCAGTTATTATTAAC----- 591
Db 161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180
QY 592 -----GTTATTAT 600
Db 181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200
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Db 201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220
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QY 781 ATGACATGTGTCATTCGACATCGTGTGCTAGAACTTCTGACGCTACTCAATGTCTCCA 840
Db 261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280
QY 841 TCTGTGACTTGTCTACTCAGCAGAAATGATTCAATACGACTACTTGCATCTTGGGT 900
Db 281 PheCysAlaLeuPheThrHisAspGluTyrArgGlnTyrAspTyrLeuGlnSerLeuGly 300
QY 901 AAGTACTACGTTACGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320
QY 961 AAGCAATTGATTGCTAGATTGACTCACTCTCCAGTTTCAAGACACACACTTCTACTAC 1020
Db 321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340
QY 1021 ACTTGGACTCTAACCCAGCTACTTCCCATTGAAAGCTACTTGTGACGTGACTTCTCT 1080
Db 341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360
QY 1081 CAGCAACAACCTATGTGTTCTATTTCTCGCTTTGGGTTTGTACAGGCTACTAAGCCA 1140
Db 361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380
QY 1141 TTGCTACTACTTCTGTGTAATCTATTGAAGAACGACGCTTACTCTGCTTCTGACT 1200
Db 381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTyrThr 400
QY 1201 GTTCCATTCCCTGCTAGAGCTTACGTGTAATGATGCAATGCTGAAGCTGAAAGGAACCA 1260
Db 401 ValProPheGlyAlaArgAlaTyrValGluMetGlnCysGlnAlaGluLysGluPro 420
QY 1261 TTGGTTAGAGTTTGGTTAACGACAGAGTTGTTCCCATTTGACCGGTTGTGCTGTGACA 1320
Db 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440
QY 1321 TTGGGTAGATGTAAGAGACGACTTGGTTGAAGGTTTGTCTTCGCTAGATCTGCTGCT 1380
Db 441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGCAAGAAATGTTTCGCT 1401
Db 461 AsnTyrAlaGluCysPheAla 467
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RESULT 5

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US-09-634-493A-2
; Sequence 2, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13219
; CURRENT APPLICATION NUMBER: US/09/634,493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121,425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-09-634-493A-2
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Alignment Scores:
Pred. No.: 2,69e-204 Length: 467
Score: 2170.00 Matches: 416
Percent Similarity: 87.68% Conservative: 11
Best Local Similarity: 85.42% Mismatches: 20
Query Match: 87.29% Indels: 40
DB: 4 Gaps: 2

US-09-488-265B-30 (1-1404) x US-09-634-493A-2 (1-467)
QY 1 ATGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60
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QY 61 GCCTGGGCTCTCGTGGTAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40
QY 121 TTCGCCAGAAATTTCTCACTTGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180
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QY 41 PheProGluIleSerHisLeuIrrPglyGlnTyrSerProTyrPheSerLeuGluAspGlu 60
Db 41 PheProGluIleSerHisLeuIrrPglyGlnTyrSerProTyrPheSerLeuGluAspGlu 60
QY 181 TCTGCTATTCTCCACACGCTTCCAAAGGCTTGTAGAGTTTACTTTCGTTCAAGTTTGTCT 240
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QY 241 ACACACGGTCTAGATACCCACTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla 97
QY 301 GCTATTCAAAGAACGCTACTGCTTTCAAAGGCTTGTAGAGTTTACTTTCGTTCAAGACTTACAAC 360
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QY 361 TACACTTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 101 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120
QY 421 ATTAAGTTCTACAGAGATACAAAGGCTTGGCTAGAGAGATGTTTCCATTCTCACTGAGCT 480
Db 121 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 140
QY 481 TCTGGTCTGACAGAGCTTATTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160
QY 541 AAGTTGGTGCACCCAGGTCCTAACCCACACAGCTTCTCCAGTCTTCCAGTCTTAAAC 591
Db 161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180
QY 592 592
Db 181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200
QY 601 CCAGAAAGTGTGGTTTACAAACACACTTTGGACCCAGGTTTGTGCTGCTGCTGCTGCTGCTGCT 660
Db 201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220
QY 661 TGTGAATGGGTGACGACGCTTGAAGCTAACTTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
QY 721 GCTAGATTGGAAGCTCCTTCCAGGCTGTTTACTTCACTGACGACGACGCTTGTGTAACITG 780
Db 241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260
QY 781 ATGGACATGTCTCCATTCACACACTGTTGCTAGAACCTTCTGACGCTACTCAATGTCTCCA 840
Db 261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280
QY 841 TCTGTGACTTGTCTCACTCACGACCAATGATTCATACGACTACTTGAATCTTGGGT 900
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Db 301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320
QY 961 AACGAATGATTGCTAGATTGACTCCTCCTCAGTTCAGGTTCAAGACCACCTTCTACTAACCC 1020
Db 321 AsnGluLeuLeuAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340
QY 1021 ACTTTGGACTCTAACCCAGCTACTTCCCATTCAGCTGCTGCTGCTGCTGCTGCTGCT 1080
Db 341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360
QY 1081 CAGCACAACACTATGTTTCTATTTCTTCGCTTGGGTTTGTACAAGGCTACTAAGCCA 1140
Db 361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380
QY 1141 TTGCTACTACTCTGTTGTAATCTATTGAAGAACTGACGGTTACTCTGCTCTTGGACT 1200
Db 381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400
QY 1201 GTTCCATTCGCTAGAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAAGCAACCA 1260
Db 401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro 420
QY 1261 TTGGTTAGAGTTTGGTTAAACAGACAGAGTGTTCATTCGACGGTGTGGTGTGACAA 1320
Db 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440
QY 1321 TTGGGTAGATGTAAAGACAGACACTTCGTTGAAGCTTGTCTTCGCTAGATCTGGTGT 1380
Db 441 LeuGlyArgCysLysArgAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGAAGATGTTTCGCT 1401
Db 461 AsnTrpAlaGluCysPheAla 467

RESULT 6
US-08-868-435-33
Sequence 33, Application US/08868435
Patent No. 6291221
GENERAL INFORMATION:
APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/868.435
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/744,231
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/DOCKET NUMBER: Case Docket 9339
TELEPHONE: (201) 235-4205
TELEFAX: (201) 235-2363

INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: misc_feature
LOCATION: 104
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 119
OTHER INFORMATION: /note="potential N-glycosylation site"
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LOCATION: 205
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 228
OTHER INFORMATION: /note="potential N-glycosylation site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 374
OTHER INFORMATION: /note="potential N-glycosylation site"
US-08-868-435-33
Alignment Scores:
Pred. No.: 1,29e-176 Length: 465
Score: 2888.00 Matches: 359
Percent Similarity: 84.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
Gaps: 2
US-09-488-265B-30 (1-1404) x US-08-868-435-33 (1-465)
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Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 6: GCCTGGGTCCTCGTGAATCTCTACTCTGTGACACICTGTGACGGTGTACCAATGT 120
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 121 TTCCAGAAATTTCTCCTACTGTCGCTGTCATCTCTCCATTCCTCTCTTGGCTGACGAA 180
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY 181 TCTGCTATTTCTCCAGACGTTCCAAAGGGTTGTAGAGTIACTTTCTCAAGTTTCTGCT 240
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 AGACACGGTGTAGATACCAACTTCTCTCCGCTCTAAGGGGTACTCTGCTTTCATTGAA 300
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysLysLysLysLysLysLysLysLys 99
QY 301 GCTATTCAAAAGAACGCTACTGCTTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC 360
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGCTGCGTGAACAACAATGTTTAACTCTGT 420
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAAGTCTACACAAGATACAAAGCTTTGGCTAGAGAAGAITGTTCCATTCATTAGAGCT 480
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159

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QY 481 TCTGCTTCACAGAGTTATTCGTTCTGCTGAAAGTTCATTAITGAAGTTTCCCAATTCGT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGluAla 179
QY 541 AAGTTGCTCACCAGCTGCTAACCCACACCAAGCTCTCCAGCTTATTACGCTTATTATT 600
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
QY 601 CCAGAGGTGCTGTTTCAACAACACTTGGACACAGGGTTGTGACTGCTTTCCAGCAA 650
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATGGGTGACGACGTTGAAGCTAACTTCACTGCTGCTTTTCCGCTCCACCAATTAGA 720
Db 219 SerGlnLeuGlyAspGluAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATTGGAAGTCACTTCCAGGTTTAACCTTGACTGACCAAGACGGTTGTAACTTG 780
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGCACATGTGCTCCTCGACACTGTGTGCTAGAACCTTCTGACGCTACTCAATTTGCTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TCTGCTGACTGTTTCACTCAGCAGCAATGATTCAATACGACTACTTGCATCTTTGGGT 900
Db 279 PheCysGlnLeuPheThrHisAsnGluThrPheLysIleAsnIleLeuGlnSerLeuGly 298
QY 901 AAGTACTACGGTTACGGTGTGTAAACCCATGGGTCACGCTCAAGGTGTGGTTTCGTT 960
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QY 1021 ACTTGACTCTCAACCCAGCTACTTCCCATTTGAAGCTACTTTGACGCTGACTTCTCT 1080
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QY 1141 TTGCTACTACTTCTGTGATCTATGAGAAGCTGACGGTTACTCTCTCTTCTTGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaAlaLysGluLeuAspIleTyrSerAlaSerIlePheVal 398
QY 1201 GTTCCATTCTGCTAGAGCTTACGTTGAAATGATGCAATGGAAGCTGAAAAGGAACCA 1260
Db 399 ValProPheGlyAlaArgAlaIlePheGluThrMetGlnCysLysSerGluLysGluPro 418
QY 1261 TTGGTTAGAGTTTGGTTIACGACAGAGTTTCCATTGACCGGTTGTTGGTGTGACAG 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValIleProLeuHisGlyCysAspValAspLys 438
QY 1321 TTGGGTAGATGTAAGACAGCAGCTTCTGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerIlePheAlaArgSerGlyGly 458
QY 1381 AACTGGGAAGAATGTTTCGCT 1401
Db 459 AsnIlePheGlyGlyCysPheSer 465
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RESULT 7

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US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
; GENERAL INFORMATION:
; APPLICANT: Van Loon, Adolphus
; APPLICANT: Mitchell, David
; TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
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Alignment Scores:
Pred. No.: 1,29e-176 Length: 465
Score: 1888.00 Matches: 359
Percent Similarity: 84.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
DB: 4 Gaps: 2
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US-09-488-265B-30 (1-1404) x US-08-744-231-33 (1-465)
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QY 61 GCCTTGGGTCCTCGGTGAACCTCTCTGACACTGTGTGACGGTGGTTACCAAGT 120
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QY 301 GCTATTCAAAGACGCTACTGCTTTCAAAGGTAAGTACGCTTCTTGAAGACTTACAA 360
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Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAAGTCTACAGAGATACAGGCTTTGGCTAGAAAGATTGTTCCATTTCATTAGACT 480
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QY 481 TCTGTTCTGACAGAGTATTCTCTCTGCTGAAAGTTTCATGAAGTTTCCAACTGCT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGlnGlyPheGlnGlnAla 179
QY 541 AAGTTGGGTGACCCAGGCTTAACCCACCAAGCTTCCAGTTATTAAAGTTATTACT 600
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIlele 198
QY 601 CCAGAGGTGCTGGTTACAAACACTTTGGACCAAGCTTTGGTACTGCTTTCGAGAA 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
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Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGGACATGTCCTCACTGACACTTCTGACAGCTTCTGACGCTACTCAACTGCTTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TTCTGTGACTTCTCACTCACAGCAATGGATTCAATACGACTTCTGCAATCTTTGGGT 900
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Db 459 AsnTrpGlyGluCysPheSer 465
RESU:T 8
US-09-044-718-78
: Sequence 78, Application US/09044718
: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: CURRENT FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 78
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-09-044-718-78
Alignment Scores:
Pred. No.: 1,29e-176 Length: 465
Score: 1898.00 Matches: 359
Percent Similarity: 84.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
DB: 4 Gaps: 2
US-09-488-265B-30 (1-1404) x US-09-044-718-78 (1-465)
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Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 61 GCCTTGGGTCCTCGTAACTCTCTACTCTGTGACACTGTTTCACGCTTTCACCAATGT 120
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QY 181 TCTGCTATTCTCCAGAGCTTCCAAAGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
Db 60 LeuSerValSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
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Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLysLeuValThr 99

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QY 301 GCTATTCAAAGACGCTACTGCTTTTCARGGSTAAGTACGCTTCTTGAGACTTACAC 360
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Db 239 AlaArgAlaLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGACATGTTCCATTCGACACTGTTGCTAGAACTTCTCACGCTACTCAATGTCCTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TTCTGTGACTTGTCTACTCAGCAGGATGATTCATACCACTACTTGCATCTTGGGT 900
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysTyrAsnTyrLeuGlnSerLeuGly 298
QY 901 AAGTACTACGGTTACGGTGTGTGTAACCCATTGGGTCCAGCTCAAGGTGTGTTGCT 960
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 961 AAGCAATTGATTCTAGATTGACTCAGCTCCAGCTTCAACACACACACTTCTACACACCAC 1020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGGACTCTAACCCAGCTACTTTCCCATTTGAAGCTACTTGTACGCTGACTCTCT 1080
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1081 CAGCACAACTATGTTCTTCTATTTCTTCGTTTGGGTTTGTACACGCTACTACGCCA 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyTyrGluPro 378
QY 1141 TTGCTACTACTTCTGTTGAATCTATTGAGAAGACTGACCGTTACTTCGTTCTGTTGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTyrpVal 398
QY 1201 GTTCCATTCTGCTAGAGCTTACGTTGAATGATGAATGTGAAGCTGAAAAGGAACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
QY 1261 TTGTTTAGAGTTTGGTTAAACAGACAGAGTTGTTCCATTTGCACGCTTGTGTTGACAAG 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY 1321 TTGGGTAGATTGTAAGACAGACACTTGGTTGAAGGTTTGTCTTTCGCTAGATCTGTTGGT 1380
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTyrpAlaArgSerGlyGly 458
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QY 1381 AAC1GGGAAGAATGTTGCT 1401
Db 459 AsnTrpGlyGluCysPheSer 465

RESULT 9
US-09-636-499-6
: Sequence 6, Application: US/09636499
: Patent No. 6475762
: GENERAL INFORMATION:
: APPLICANT: Stafford, Christian F.
: APPLICANT: Trinci, Anthony P.J.
: APPLICANT: Brookman, Jayne L.
: TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
: TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
: FILE REFERENCE: GC586-2
: CURRENT APPLICATION NUMBER: US/09/636,499
: CURRENT FILING DATE: 2000-08-11
: PRIOR APPLICATION NUMBER: US 60/148,960
: PRIOR FILING DATE: 1999-08-13
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: FastSEQ for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 465
: TYPE: PR1
: ORGANISM: Aspergillus fumigatus
US-09-636-499-6

Alignment Scores:
Pred. No.: 1,29e-176 Length: 455
Score: 1888.00 Matches: 359
Percent Similarity: 84.37% Conservative: 35
Best Local Similarity: 76.87% Mismatches: 71
Query Match: 75.95% Indels: 2
DB: 4 Gaps: 2

US-09-488-265b-30 (1-1404) x US-09-636-499-6 (1-465)

QY 1 ATCGCGGTCTGCTGCTGCTATGCTCCATTGCTCCACCTTCTCGGTGCCACATCGGTACC 60
Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 61 GCTTGGGTCTCGTGGTAACTCTCTCTGACACTGTTGACGGTGGTACCAATGT 120
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 121 TCCCAGAAATTTCTCACTTCTGCGGTACATACTCTCCATTCTCTTCTTGGCTCAGAA 180
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY 181 TCTGCTATTCTCCACACTTCCAAAGGTTGTAGAGTTACTTCTTCAAGTTTGTCT 240
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 AGACAGGCTGTAGAPACCAACTTCTCTGCGCTAAGCGTACCTCTCTTGAATGAA 300
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysTyrLysTyrLysLysLeuValThr 99
QY 301 GCTATTCAAAGACCTTACTCTTCAAGGTAAGTACGCTTCTTGAGACTTACAC 360
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 361 TACACTTTGGGTGCTGACGACTTACCTCCATTCCGGTGAACAACAAATGGTTAACTCTGT 420
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAAGTTCTACAGAGATACAGGCTTGGCTAGAAAGATTGTTCCATTCATTAGACT 480
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 481 TCTGGTCTCACAGAGATTATTGCTTCTGCTGAAAAGTTCATTGAAAGTTTCCAACTGCT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlnGlnAla 179
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QY 541 AAGTTGGTGCACCGAGTGTCAACCCACACACAGCTTCCAGTTATTAAAGCTTATTAT 600
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAaAlaProAlaIleSerValIlelle 196
QY 601 CCAGAAGTGTGGTTTACACACACTTTGGACCGGTTGTGTACTGCTTTCGAAGAA 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 216
QY 661 TCTGAATGGGTGACGACGCTCAAGCTAACTTCACTGCTGTTTCGCTCCACCAATAGA 720
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATTGAAGCTCACTTGCAGGTGTAACTTGACTGACGACGAGAGAGTGTAACTG 780
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValSerLeu 258
QY 781 ATGGACATGTCCTCCATTCACACTGTTCTAGAACTTCTGACGCTACTCAATTGTCTCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TCTGTGACTTGTCTACTCAGCAGCAATGATTCATCAATACGACTTCTGCAATCTTGGT 900
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnThrLeuGlnSerLeuGly 298
QY 901 AAGTACTACGGTACGGTGTGTAACTGAGTGTGGTCCAGCTCAAGGTGTGGTTCGTT 960
Db 299 LysTyrTyrGlyTyrGlyAaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 961 AACGAATGATTCAGTATGACTCAGCTCCAGTTCAGACCCACACATCTACTAACCAC 1020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGGACTTAACCCAGCTACTTCCCATTTGACGCTACTTTGTAGCTGACTTCTCT 1080
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1081 CAGGACAACTAAGTGTCTATTCTTCTGCTTGGTGTGTGACAGGCTACTAAGCA 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
QY 1141 TTGCTCTACTACTTCTCTCAATCTATTGAAGAACTGACGGTTACTCTGCTTCGTGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
QY 1201 GTTCCATTGCTGCTAGAGCTTACGTTGAATGATGCAATGTGAAGCTGAAAGGAACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
QY 1261 TTGGTTAGAGTTTGGTTAACACAGAGTTGTTCATCCACGGTGTGGTGTGACAAAG 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValProLeuHisGlyCysAspValAspLys 438
QY 1321 TTGGTTAGATGTAAGAGACGACTTCTGTTGAAGTTTCTCTTTCGCTAGATCTGGTGT 1380
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
QY 1381 AACTGGGAAGATGTTTCCT 1401
Db 459 AsnTrpGlyGluCysPheSer 465
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RESULT 10
US-09-273-871A-8
; Sequence 8, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618,500-US
; CURRENT APPLICATION NUMBER: US/09/273,871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806

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; PRIOR FILING DATE: 1998-06-19  
; PRIOR APPLICATION NUMBER: PA 1998 01176  
; PRIOR FILING DATE: 1998-09-18  
; PRIOR APPLICATION NUMBER: PA 1999 00091  
; PRIOR FILING DATE: 1999-01-22  
; PRIOR APPLICATION NUMBER: 60/080,129  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/090,675  
; PRIOR FILING DATE: 1998-06-25  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: fastseq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 465  
; TYPE: PRT  
; ORGANISM: Aspergillus fumigatus  
US-09-273-871A-8  
  
Alignment Scores:  
Pred. No.: 1,29e-176 Length: 465  
Score: 1888.00 Matches: 359  
Percent Similarity: 84.37% Conservative: 35  
Best Local Similarity: 76.87% Mismatches: 71  
Query Match: 75.95% Indels: 2  
Gaps: 2  
DB: 4  
US-09-488-265B-30 (1-1404) x US-09-273-871A-8 (1-465)  
  
QY 1 ATCGCGCTGTTGCTGCTGCTACTGCTCCATTCGCCACCTGTTGTCGGTTCCACATCCGGTACC 60  
Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaThrLeuLeuSerGlyArgValSerAla 20  
QY 61 GCCTTGGTCTCCTCGTGTAACTCCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGT 120  
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39  
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Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59  
QY 181 TCTGCTATTTCTCCACAGCTTCCAAAGGTTGTAGAGTTACTTCTGCTTCAAGTTTGTCT 240  
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79  
QY 241 AGACACGGTGTGATACACCAACTCTCTGCGGTCTAAGCGGTACTCTGCTTTGATTTAA 300  
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLysLysValThr 99  
QY 301 GCTATTCAAAGAACGCTACTGCTTTCACAGGTAAAGTACGCTTCTTGAAGACTTACAAC 360  
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTrpAsn 119  
QY 361 TACACTTTGGTGTGACGACTTGCATCCATTCGCTGAACCAACAAATGGTTAACTCTGT 420  
Db 120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139  
QY 421 ATTAAGTTCTACACAAATACACAGCTTTGGCTAGAAAGATTGTTCCATTCATTAGACT 480  
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159  
QY 481 TCTGTTCTGACAGATTATTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179  
QY 541 AAGTTGGTGTGACGCTGCTTAAACCCACACAGCTTCTCCAGTTATTAAAGTTATTATT 600  
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIlelle 198  
QY 601 CCAGAAGTGTGCTGTACACACACACTTTCGACCCAGCTTGTGTACTGCTGCTTTCGAGAA 660  
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218  
QY 661 TCTGAATGGGTGACGAGCTTGAAGCTAAGTCTCACTGCTGCTTTCGCTCCACCAATAGA 720  
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
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Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 961 AACGAATGATGCTAGATCACTCACTCTCCAGTTCACAGACACACTTCTACTAACCCAC 1020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGGACTCTAACCCAGCTACTTCCCATTTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1081 CACGACAACTATGTTTCTATTTCTTCGCTTTGGGTTTGTACACGGTACTACACCCA 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
QY 1141 TTGTCTACTTCTCTGTTGAATCTATTGAACAACTACGCTTACTCTCTCTCTCTGACT 1200
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QY 1201 GTTCCATTGCTGTAGAGCTTACGTTTCAATGATGCAATGTGAAGCTGAAAGGAACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluSer 418
QY 1261 TTGTTAGAGTTTGGTTACGACAGAGATTTGTTCCATTCACGGTTCTGGTGTGTGACAG 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY 1321 TTGGGTAGATTAAGAGAGAGAGCTTCTGTTGAAGTTTGTCTTTCGCTAGATCTGGTGGT 1380
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QY 1381 AACTGGGAAGAAATGTTTCGCT 1401
Db 459 AsnTrpGlyGluCysPheSer 465
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RESULT 12

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US-09-044-718-79
; Sequence 79, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCH, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-79
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Alignment Scores:
Pred. No.: 9,86e-176 Length: 465
Score: 1879.00 Matches: 358
Percent Similarity: 84.15%
Best Local Similarity: 76.66% Conservative: 35
Query Match: 75.58% Indels: 2
DB: 4 Gaps: 2
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US-09-488-265B-30 (1-1404) x US-09-044-718-79 (1-465)

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QY 61 GCCTTGGGTCTCGTGGTAACTCTCACTCTTGTGACACTGTTGACGGTGGTACCAGTGT 120
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QY 121 TTCCCAAGAAATTTCTCACTTGTGGGTACATCTCTCCCATTTCTCTCTTGTGCTACGAA 180
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY 181 TGTGCTATTTCCTCCAGACGCTTCCAAAGGCTTTAGAGTTACTTTCGTTCAAGTTTGTCT 240
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 AGACACGGTGTAGATACCACTTCTCTCGCTCTAAGCGCTACTCTCTCTTGTATTGAA 300
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysLysLysLysLysLys 99
QY 301 GCTATTCAAAAAGAACGCTACTGCTTTCAGAGGTAGTAGCTTCTTGAAGACTTACAAAC 360
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 361 TACACTTTGGGTCTCACCAGCTTGACTCCATTCGGTGGTGAACAAATGTTAACTCTGTG 420
Db 120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 421 ATTAAGTTCTACGAAGATACAGAGCTTTGGCTAGAAAGATTGTTCCATTCTTAGAGCT 480
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 481 TCTGTTCTGACAGAGATTATGCTCTGCTGCTGAAAGTTCAATTGAAGTTTCCAACTGCT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGlyLysPheIleGluGlyPheGlnAla 179
QY 541 AGCTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAACTGTTATT 600
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
QY 601 CCAGAAAGTGTGCTTACAAACACTTTGGACCACTTGTGTACTGCTTCTGGAAGAA 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATTTGGTGACGAGCTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCAATTAGA 720
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATTGGAAGCTCACTTGCAGGTGTAACTTCAGTCACTGACGACAGACGTTGTTA 780
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGGACATGTGCTCATTCGACACTGTTGCTAGAACTTCTGACGCTACTCAATGTCTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TTCTGTGACTTGTTCCTACTCAGCAGCAATGATTCATATAGACTACTTGCATCTTTGGGT 900
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298
QY 901 AAGTACTACGTTACGTCGTCGTAACCCACTTGGGTCCAGCTCAAGCTCTTGGTTCGTT 960
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 961 AACGAATGATGCTAGATTGACTCACTCTCCAGTTCACAGACACACTTCTACTAACCCAC 1020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGGACTCTAACCCAGCTACTTCCCATTTGAACGCTACTTTGTACGCTGACTTCTCT 1080
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1081 CACGACAACTATGTTTCTATTTCTTCTGCTTGGGTGTTGTACACGGTACTACGCTACC 1140
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluGly 378
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2b	1	MetValThrLeuThrPheIleuLeuSerAlaAlaTyrLeuLeuSerGlyA-gValSerAla	20
QY	61	GGCTGGGTCCTGGTAAATTCACACTCTCTGCACACTGTTGACGGGTGTACCAATGT	120
Db	21	AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys	39
QY	121	TTCCAGAGAATTCTCAGTCTGGGGTACACTCTCCATACACTCTCTTTGGGACGACAA	180
Db	40	SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu	59
QY	181	TCGTATTCTCCAGACGGTCCAGACGACTAGAGTTACTTCGTTCGAAGTTTCTCT	240
Db	60	LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer	79
QY	241	AGACAGGGTCTAGATACCAACTTCTTCGCGCTTAAGGCTTACTCTGCTTCATTCAT	300
Db	80	ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr	99
QY	301	GCTATTCAAAGAACGCTACTGCTTTCAAGGGTAAGTACGCTTCTTTGAAGACTTACAAC	360
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QY	361	TACACTTTGGTGCTGACGACTTGACTCCATTCCGTGAAAACCAATGGTTAACTCTGGT	420
Db	120	TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnLeuValAsnSerGly	139
QY	421	ATTAAAGTTCTACAGAAGATACAGGCTTTCGCTAGAAAGATTGTTCCATTCATTAGAGCT	480
Db	140	IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla	159
QY	481	TCGTGGTCTGACAGAGTTATTCGCTTCGTGAAAAGTTTCATTGAAGTTTCCCAATCTGCT	540
Db	160	SerGlySerAspArgValIleAlaSerGlyGlnLysPheIleGluGlyPheGlnGlnAla	179
QY	541	AAGTTGGCTGACCGAGTTCTCAACCACACACGAGCTTCTCCAGTTATTAACGTGATCAIT	600
Db	180	LysLeuAlaAspProGlyAla---ThrAsnArgAlaAlaProAlaIleSerValIleIle	198
QY	601	CCAGAAGATCCGGTTACAACAACACTTTGGACCACGCTACTTCTACTGCTTTCGAAGAC	660
Db	199	ProGlnSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla	218
QY	661	TCCTCAATTAGTGTGACGACGTTGAAGCTTAACCTTCACCTGCTTGTTCGCTCCAGCTTAGA	720
Db	219	SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg	238
QY	721	GCTAGATTGAAGCTGACTTCGACAGTGTTACTTTTGACTGACGAAGACGTTGTTACTHTG	780
Db	239	AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu	258
QY	781	ATGCACATGTCCATTGCACTGTCCGTAGAACITTCGACGCTACTGAATTCGTCCTCA	840
Db	259	MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro	278
QY	841	TTCTGTGCTTTGTTCTACTCAGCAGAAATGGATCCAAATACGACTACTTCGAAAAGCTGGGT	900
Db	279	PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly	298
QY	901	AAGTACTACGGTTACGGTGTGGTTAACCCATTGGGTCCAGCTCAAGGTGTGGTTTCGCT	960
Db	299	LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr	318
QY	961	AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTCTACTAACCAC	1020
Db	319	AsnGluIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer	338
QY	1021	ACTTTGACTCTTAACCCAGCTACTTTCCCAATTGGAACGCTACTTTGTACGGTGTCTCT	1080
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QY	1081	CACGACAACACTATGATATCTATTTCTTCGTTTGGGTTTGTACACACGGTACCAAGCCA	1140
Db	359	HisAspAsnSerMetValSerIlePhePheAlaLeuGlyValLeuTyrAsnGlyThrGluPro	378

RESULT 10
US-10-062-848-80

Db	180	LysLeuAlaAspProGlyAla	----	ThrAsnArgAlaAlaProAlaIleSerValIle	198	
QY	601	CCAGAAGGATCCGGT	TACAACAACAC	ATTGGACCACGGT	ACTTGTACTGCTTTCGAAGAC	660
Db	199	ProGlnSerGluThr	PheAsnAsnThr	LeuAspHisGlyValCysThr	LysPheGluAla	218
QY	661	TCTCAATTTAGGT	GACGACGGTTGAAGCT	TAACTTCACTGCTTTGTTCGGT	TCCAGCTATTAGA	720
Db	219	SerGlnLeuGlyAsp	GluValAlaAlaAsn	PheThrAlaLeuPheAlaPro	AspIleArg	238
QY	721	GCTAGATTGAAAGT	GACTTCCGACGGT	TTACTTTTGACT	GACGAAAGACGTGTTTACT	780
Db	239	AlaArgAlaGluLys	HisLeuProGlyValThr	LeuThrAspGluAspValValSerLeu		258
QY	781	ATGCACATGTGT	CCATTTCGACACT	GTGCGTAGAAC	TTCTGACGGTACTGAATTCGTCCTCA	840
Db	259	MetAspMetCysSer	PheAspThrValAlaArgThr	SerAspAlaSerGlnLeuSerPro		278
QY	841	TTCTGTGCTTTGT	TCTACTCAGCAGAA	TGGATCCAAATACGACT	ACTTTCGAAAAGCTTGGGT	900
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QY	901	AAGTACTACGGTT	ACGGTGTGGTGA	ACCATTGGGTCCAGCTCAAGGTGTGTGGTT	TCGCT	960
Db	299	LysTyrTyrGlyTyr	GlyAlaGlyAsnPro	LeuGlyProAlaGlnGlyIleGlyPheThr		318
QY	961	AACGAATTGATT	TGTAGATTGACT	CACTCTCCAGTTCAAGACCA	CACACTTCTACTAATCCAC	1020
Db	319	AsnGluLeuIleAla	ArgLeuThrArgSerPro	ValGlnAspHisThrSerThrAsnSer		338
QY	1021	ACTTTGACTCT	TAACCCAGCTACTTTCCCAT	TGAAACGCTACTTTGTACGGT	GACTTCTCT	1080
Db	339	ThrLeuValSerAsn	ProAlaThrPhePro	LeuAsnAlaThrMetTyrValAspPheSer		358
QY	1081	CACGACAACACT	ATGATATCTATTTCT	TCGTTTGGGTTTGTACAACGGT	TACCAAGCCA	1140
Db	359	HisAspAsnSerMet	ValSerIlePhePheAlaLeuGlyValLeuTyrAsnGlyThr	GluPro		378

D _B	299	LysTyrIrrGlyTyrglyAlaArgAsnProLeuglyProAlaGlnGlyIleGlyPheThr	318
D _B	961	AAGCAATTGGCTACGATTSACTCCTCCAGTTCCAAGACCACACTTCCTACTAACCCAC	1020
Q _Y			
D _B	319	AsnGluLeuileAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer	338
Q _Y			
D _B	1021	ACTTGGACTCTAACCACGACTCTCCCATTTGAACGCTACTTGTCAGCGTACTCTCT	1080
Q _Y			
D _B	339	ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMettyrValAspPheSer	358
Q _Y			
D _B	1081	CACGACAACACIATGATATCTATTCTTCGCTTTGGGTTGTACACGGTACCAAGCCA	1140
Q _Y			
D _B	359	HISAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTrpAsnGIvThrGluPro	378
Q _Y			

Qy	1081	CAGCAGACACTATGATATCTATTTCTTCGCTTTGGTTTGTCACACGGTACCAAGCCA	1140
Dd	339	inrLeuValSerAsnProAlaIatInrPheProLeuAsnAlaInrMetIlyValAspPheSer	350
Dd	359	HisAsnSerMetValSerIleIlePhePheAlaLeuGlyLeuValAsnGlyThrGluPro	378

[illegible]


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; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-12

Alignment Scores:
Pred. No.: 5,79e-151 Length: 449
Score: 1857.50 Matches: 347
Percent Similarity: 87.05% Conservative: 36
Best Local Similarity: 78.86% Mismatches: 56
Query Match: 74.90% Indels: 1
DB: 15 Gaps: 1

US-09-488-265b-28 (1-1404) x US-10-062-848-12 (1-449)
QY 82 TCTCACTCTTGTGACACTGTTGACGGTGGTTACCAATGTTTCCAGAAATTTCTCACTTG 141
DB 11 SerLysSerCysAspThrValAspLeuGlyTyrGlnCysSerProAlaThrSerHisLeu 30
QY 142 TGGGTACTACTCTCCATCTCTCTTTGGCAGCAGCAATCGTATTTCTCCAGAGCTT 201
DB 31 TrpGlyGlnTyrSerProPheSerLeuGluAspGluLeuSerValSerSerLysLeu 50
QY 202 CCAGACGACTCTAGATTACTTTCGTTCAAGTTTGTCTACACAGCGTGTAGATACCCA 261
DB 51 ProLysAspCysArgIleThrLeuValGlnValLeuSerArgHisGlyAlaArgIlePro 70
QY 262 ACTTCTCTCGCTCTAAGGCTTACTCTCTGTTGATTGAAGCTATTCAAAAGACGCTACT 321
DB 71 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 90
QY 322 GCTTTCAGGGTAAGTACGCTTCTTGAAGACTTACAACTACACTTTGGGTGCTGACGAC 381
DB 91 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAspAsp 110
QY 382 TTGACTCCATTCGGTGAACAACTGTTAACTCTGTTAACTGTTAACTCTCAGAGATAC 441
DB 111 LeuThrProPheGlyGluGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 130
QY 442 AAGCTTTGGCTAGAAAGATTGTTCCATTCATTAGAGCTTCTGTTCTGACAGAGTATT 501
DB 131 LysAlaLeuAlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIle 150
QY 502 GCTTCTGCTGAAGACTTCAATGAAGTTTCAATGCTGCTAGTTGGTGGTACCCAGGTTCT 561
DB 151 AlaSerGlyGluLysPheIleGluGlnGlnAlaLysLeuAlaAspProGlyAla 170
QY 562 CAACACACCAAGCTTCTCCAGTTTCACTTACGATTCATTCAGAGGATCCGGTTACAC 621
DB 171 ---ThrAsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 189
QY 622 AACACTTTGGACCGGCTACTGTGTTGCTTCCAGACTCTGAATTAGGTGACGAGCTT 681
DB 190 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 209
QY 682 GAAGCTACTTCACTGCTTGTTCGCTCCAGCTATTAGAGCTAGATTGGAAGCTGACTTG 741
DB 210 AlaAlaAsnPheThrAlaLeuPheAlaProAspIleArgAlaAlaGluLysHisLeu 229
QY 742 CCAGGTGTTACTTTCAGTACGACGACCTGTTTACTTGTATGATGGACATGTCTCCATTG 801
DB 230 ProGlyValThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAsp 249
QY 802 ACTGTGCTAGAACTTCTGACGCTACTGAATTTGTTCTCCATTTCTGCTTTGTTCACAC 861
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DB 250 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 269
QY 862 GACGAATGATCCAAATAGCACTACTTGCAGAGCTGGTAAAGTACTACGGTTACGGTGCT 921
DB 270 AsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAla 289
QY 922 GGTAAACCATTTGGTCCAGCTCAAGGTGTTGGTTTCGCTAACCAATTTGATTGCTAGATTG 981
DB 290 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuIleAlaArgLeu 309
QY 982 ACTCACTCTCCAGTTCAGACACCACTCTTACTAACCACTTTGGACTTTAACCAGCT 1041
DB 310 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 329
QY 1042 ACTTCCATTCAGACGCTACTTGTACGCTGACTTCTCTCACCACACACTATGATATCT 1101
DB 330 ThrPheProLeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSer 349
QY 1102 ATTCTCTCGCTTTGGTGTACAAAGCGTACCAAGCATTTGCTACTACTTCTGTTGAA 1161
DB 350 IlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluProLeuSerArgIleSerValGlu 369
QY 1162 TCTATTGAAGAACTGACGCTTACTCTGCTTCTTGGACTGTTCCATTCGCTGCTAGCT 1221
DB 370 SerAlaLysGluLeuAspGlyTyrSerAlaSerTyrValValProPheGlyAlaArgAla 389
QY 1222 TACGTTCAATGATGCAATGCTCAAGCTGAAAGAACCACTTGTACAGTTTGGTTAAC 1281
DB 390 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 409
QY 1282 GACAGAGTTGTTCCATTCGACGCTGTGCTGTGACAAAGTTGGTGTAGATGTAAGAGAC 1341
DB 410 AspArgValValProLeuHisGlyCysAspValAspLysLeuGlyArgCysLysLeuAsn 429
QY 1342 GACTTCGTTCAAGGTTTGTCTTTCGCTAGATCTGTTGTTAACTGGGCTGAATGTTGCT 1401
DB 430 AspPheValLysGlyLeuSerTyrAlaArgSerGlyGlyAsnTrpGlyGluCysPheSer 449
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RESULT 14

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US-10-062-848-81
; Sequence 81, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-81
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Alignment Scores:
Pred. No.: 9,64e-151 Length: 465
Score: 1855.00 Matches: 353
Percent Similarity: 83.51% Conservative: 37
Best Local Similarity: 75.59% Mismatches: 75
Query Match: 74.80% Indels: 2
DB: 15 Gaps: 2
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US-09-488-265B-28 (1-1404) x US-10-062-848-81 (1-465)
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Db 1 MetValThrLeuThrPheLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 61 GCCTTGGGTCCTCGTGAATTCCTACTCTCTGTGACACTGTTGACGGTGGTACCAATGT 120
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 121 TTCCAGAAATTTCTCAGTGTGGGTACTACTCTCCATACTCTCTTTGGCAGACGAA 180
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY 181 TCTGCTATTCTCCAGCGTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 241 AGACCGGTGCTAGATACCAACTTCTTCTGCTCTAAGGCTTACTCTCTGTTGATTGAA 300
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValInr 99
QY 301 GCTATTCAAAAGAACGCTACTGCTTCAAGGTAAGTACGCTTCTTGAAGACTTACAC 360
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 361 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACCAAAATGGTTAACTCTGT 420
Db 120 TyrThrLeuGlyAlaAspSerLeuThrAlaPheGlyGluGlnCnleuValAsnSerGly 139
QY 421 ATTAAGTCTACAGAGATACAAAGGCTTTGGCTAGAAAGATTGTTCATTCATTAGAGCT 480
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 481 TCTGGTCTCAGACAGTATTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
QY 541 AAGTTGGCTCACCAGGCTTCTCAACACACCAAGCTTCACAGTTCATTAACGTGATCAT 600
Db 180 LysLeuAlaAspProGlyAla---ThrAsnArgAlaAlaProAlaIleSerValIleLe 198
QY 601 CCAGAGGATCCGGTTACAAACACACTTTGGACCCAGGTAAGTGTACTGCTTCGGAAGAC 660
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 661 TCTGAATTAGGTGACGACGTTGAAGCTAACTTCACCTGCTTTGTCGCTCCAGCTATTAGA 720
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 721 GCTAGATTGGAAGCTGACTTGGCAGGTTGTTTACTTTGACTGACGAGACGTTGTTACTTG 780
Db 239 AlaArgAlaLysLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 781 ATGACATGTCTCCATTCGACACTGTGCTAGACTCTCTGACGCTACTGAAITGCTCCA 840
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 841 TTCTGTGCTTTGTTCTACTACGACGAAATGATCCAATACGACTACTTGCAAGCTTGGGT 900
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298
QY 901 AAGTACTACGGTTACGGTGTGTAAACCCATTGGGTCCAGCTCAAGGTGTGGTTTCGCT 960
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 961 AACGAATTGATTGCTAGATTGACTACTCTCTCCAGTTCACAGACACACTTCTTACTACAC 1020
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1021 ACTTTGGACTCTAACCCAGCTACTTCCCAATCAACGCTACTTTGACGCTGACTTCTCT 1080
Db 1080
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339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
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Db 359 HisAspAsnSerMetValSerIlePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
1141 TTGCTACTACTTCTTGAATCTATTGAAGAACTGACGGTTACTCTGCTTCTTGGACT 1200
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
1201 GTTCATTCCGCTGCTAGACTTACGTTGAATGATGCAATGTCAAGCTGAAAGAACCA 1260
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
1261 TTGGTTAGAGTTTGGTTAAGCAGACAGTGTTCATTGACGGTTGCTGTTGACAAAG 1320
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
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RESULT 15
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; Sequence 12, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; FILE REFERENCE: GC386-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 462
; TYPE: PKT
; ORGANISM: *Aspergillus niger*
US-10-229-358-12

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Score: 1851.00 Matches: 349
Percent Similarity: 84.42% Conservative: 41
Best Local Similarity: 75.54% Mismatches: 72
Query Match: 74.64% Indels: 0
DB: 15 Gaps: 0

US-09-488-265B-28 (1-1404) x US-10-229-358-12 (1-462)

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QY 61 GCCTTGGTTCCTCGTGGTAAATTCCTCAGCTTCTGTGACACTGTTGACGGTGGTACCAATGT 120
Db 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40
121 TTCCAGAAATTTCTCAGTGTGGGTACTACTCTCCATACTCTCTTTGGCAGACGAA 180
Db 41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60
181 TCTGCTATTCTCCAGCGTTCCAGACGACTTCCAGCGTACTTCTGCTCAAGTTTGTCT 240
Db 181
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Db	61	SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer	80
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Db	8:	ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu	100
Qy	301	GCTATTCAAAGAACGCTTACTGCTTTCAGAGGTAGTAGCGTTTCTTGAAGACTTACAAAC	360
Db	101	GluIleGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn	120
Qy	361	TACACTTTGGTGCTGACGACACTGACTCCATTCGGTGTGAACCAAAATGGTTAACTCTGGI	420
Db	121	TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly	140
Qy	421	ATTAAGTTCTACAGAAGATACAAAGCGTTTGGGTAGAAAGATTGTTCCATTTCATTAGAGCT	480
Db	141	IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer	160
Qy	481	TCGTGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCATTGAAGGTTTCCAAATTCGT	540
Db	161	SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr	180
Qy	541	AACTTGGCTGACCCAGGTCTCTCAACACACACAGCTTCTCCAGTTATTAACTGTGATCAT	600
Db	181	LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysLeuAspValValIle	200
Qy	601	CCAGAAGGATCCGGTTACAAACACACTTTGGACACCGGTACTTGTACTGCTTCCGAAGAC	660
Db	201	SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp	220
Qy	661	TCGTAATTAGGTGACGACGTTGAAGCTTAAGCTTCTCACTGCTTGTTCGCTCCAGCTATTAGA	720
Db	221	SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheAlaProSerIleArg	240
Qy	721	GCTAGATTGAACTGACTTCCGACGGTGTTACTTTCATTCAGCACCAACGCTTGTACTTGT	780
Db	241	GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu	260
Qy	781	ATGGACATGTGTCCATTCCAGACACTGTGCGTAGAACTTCTGACGCTACTGAATGTGCTCA	840
Db	261	MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro	280
Qy	841	TCTGTGCTTTGTCTACTCACGCAATGATGATCCAAATACGACTACTTGCAAAGCTTGGT	900
Db	281	PheCysAspLeupPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys	300
Qy	901	AACTACTACGTTACGGTGTGCTAACCCATTGGGTCAGCTCAAGGTGTGGTTCTGCT	960
Db	301	LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla	320
Qy	961	AACGAATTGATTGCTAGATTGACTCATCTCTCCAGTTCAAGACACACACTTCTACTACACC	1020
Db	321	AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis	340
Qy	1021	ACTTTGACTCTTAACCCAGCTACTTTCCCAATTGAACGCTACTTTGTACGCTGACTTCTCT	1080
Db	341	ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer	360
Qy	1081	CAGCACACACTATGATATCTATTTCTTCGCTTGGTGTGTGACACGCTGACCAAGCCA	1140
Db	361	HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro	380
Qy	1141	TTGTCTACTTCTGTTGAATCTATTGAAGAACTCACGCTTACTCTGCTCTCTTGACT	1200
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Qy	1201	GTTCCATTGCTGCTAGAGCTTACGTTGAATGATGCAATGTCACAGCTGAAAGGACCA	1260
Db	401	ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro	420
Qy	1261	TTGTTAGAGTTTTGGTTTAACGACAGAGTTGTTCCATTGACCGGTTGCTGTTTGACAAG	1320
Db	421	LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla	440

Qy	1321	TIGGGIAGAGCTACAGACAGACGACITCGTTCAAGGTTIGTCTTTCCGTACAGTCTGGTGGT	1380
Dd	441	LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyCyl	460
Qy	1381	AACTGG	1386
Dd	461	AspTrp	462

Search completed: October 3, 2003, 09:05:52
Job time : 94.6311 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: October 3, 2003, 07:48:21 ; Search time 21.0567 Seconds
(without alignments)
5642.336 Million cell updates/sec

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Perfect score: 2480
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Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 326717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=huma:4C.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09488265 -ACGN_1_1_99 -runat_03102003_074813_12239 -NCPU=6 -ICPU=3
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -FGAPOP=0.5 -FGAPOP=6
-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2408	97.1	467	4	US-09-273-871A-9 Sequence 9, Appli
2	2282	92.0	441	3	US-09-121-425-1 Sequence 1, Appli
3	2282	92.0	441	4	US-09-634-493A-1 Sequence 1, Appli
4	2270	91.5	467	3	US-09-121-425-2 Sequence 2, Appli
5	2270	91.5	467	4	US-09-634-493A-2 Sequence 2, Appli
6	1879	75.8	467	1	US-07-923-724-8 Sequence 8, Appli
7	1879	75.8	467	2	US-08-609-426A-8 Sequence 8, Appli
8	1879	75.8	467	2	US-08-374-652C-2 Sequence 2, Appli
9	1875	75.6	467	1	US-08-151-574-32 Sequence 32, Appl
10	1875	75.6	467	1	US-08-146-424-20 Sequence 20, Appl
11	1875	75.6	467	1	US-08-693-709-2 Sequence 2, Appli
12	1875	75.6	467	2	US-08-419-448-32 Sequence 32, Appl

13	1875	75.6	467	2	US-08-819-825-3 Sequence 3, Appli
14	1875	75.6	467	3	US-09-163-842-3 Sequence 3, Appli
15	1875	75.6	467	4	US-09-233-510-32 Sequence 32, Appl
16	1875	75.6	467	4	US-09-636-499-5 Sequence 5, Appli
17	1867	75.3	465	3	US-08-868-435-33 Sequence 33, Appl
18	1867	75.3	465	4	US-08-744-231-33 Sequence 33, Appl
19	1867	75.3	465	4	US-09-044-718-78 Sequence 78, Appl
20	1867	75.3	465	4	US-09-636-499-6 Sequence 6, Appli
21	1867	75.3	465	4	US-09-273-871A-8 Sequence 8, Appli
22	1863	75.1	467	4	US-09-273-871A-11 Sequence 11, Appl
23	1860	75.0	467	3	US-09-155-855-3 Sequence 3, Appli
24	1860	75.0	467	4	US-09-543-744-3 Sequence 3, Appli
25	1860	75.0	467	4	US-09-929-060-3 Sequence 3, Appli
26	1859	75.0	465	4	US-09-044-718-80 Sequence 80, Appl
27	1858	74.9	465	4	US-09-044-718-79 Sequence 79, Appl
28	1857.5	74.9	439	4	US-09-044-718-3 Sequence 3, Appli
29	1857.5	74.9	449	4	US-09-044-718-12 Sequence 12, Appl
30	1855	74.8	465	4	US-09-044-718-81 Sequence 81, Appl
31	1851	74.6	462	4	US-09-636-499-12 Sequence 12, Appl
32	1845	74.4	469	4	US-09-044-718-82 Sequence 82, Appl
33	1839	74.2	466	3	US-08-866-435-35 Sequence 35, Appl
34	1839	74.2	466	4	US-08-744-231-35 Sequence 35, Appl
35	1835.5	74.0	463	3	US-08-868-435-29 Sequence 29, Appl
36	1835.5	74.0	463	4	US-08-744-231-29 Sequence 29, Appl
37	1835.5	74.0	463	4	US-09-273-871A-10 Sequence 10, Appl
38	1833	73.9	444	4	US-09-044-718-6 Sequence 1, Appli
39	1820.5	73.4	447	4	US-09-044-718-6 Sequence 6, Appli
40	1818	73.3	443	3	US-09-155-855-1 Sequence 1, Appli
41	1818	73.3	443	4	US-09-543-744-1 Sequence 1, Appli
42	1818	73.3	443	4	US-09-929-060-1 Sequence 1, Appli
43	1813	73.1	443	3	US-09-155-855-2 Sequence 2, Appli
44	1813	73.1	443	4	US-09-543-744-2 Sequence 2, Appli
45	1813	73.1	443	4	US-09-929-060-2 Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-273-871A-9

; Sequence 9, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618 500-US
; CURRENT APPLICATION NUMBER: US/09/273.871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080.129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090.675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-09-273-871A-9

Alignment Scores:
Pred. No.: 2.7e-236 Length: 467
Score: 2408.00 Matches: 457
Percent Similarity: 98.50% Conservative: 3

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Best Local Similarity: 97.86% Mismatches: 7
Query Match: 97.10% Indels: 0
DB: 4 Gaps: 0

US-09-488-265B-28 (1-1404) x US-09-273-871A-9 (1-467)

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DB 21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyGlyCys 40
QY 121 TTCCCAAGAAATTTCTCACTTGTGGGTACCTACTCTCCATCTTCTCTTTGGCAGACGAA 180
DB 41 PheProGluIleSerHisLeuTrpGlyGlnTySerProTyPheSerLeuGluAspGlu 60
QY 181 TCTGCTATTTCTCCAGAGTTCACAGAGCTGTAGAGTTCCTTTCGTTCAAGTTTGTCT 240
DB 61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 60
QY 241 AGACACGGTGTACATACCAACTTCTTCCGCTCTAAGCTTACTCTGCTTTGATGAA 300
DB 81 ArgHisGlyAlaArgTyProThrSerLysSerLysAlaTySerAlaLeuIleGlu 300
QY 301 GCTATTCAAGAAACGCTACTCTTCAAGGTAAGTACGCTTCTTGAAGACTTACAAAC 360
DB 101 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyAlaPheLeuLysThrTyAsn 120
QY 361 TACACTTGGGTGCTGAGGACTTCACTCCATTCGGTGAACCAATGGTTACTCTGGT 420
DB 121 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 140
QY 421 ATTAAGTCTTACAAAGATACAAAGCTTGGCTAGAAGATTGTTCATTCATTAGAGCT 480
DB 141 IleLysPheIleArgArgTyLysAlaLeuAlaArgLysIleValProPheIleArgAla 160
QY 481 TCTGGTCTCAGAGATTATGCTCTGCTGAAAGTTTCATGAAGTTTCCAACTCTGCT 540
DB 161 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 180
QY 541 AAGTGGCTGACCAAGTCTTCAACCAACCAACGCTTCTCCAGTTATACGGTATCAAT 600
DB 181 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspValIle 200
QY 601 CCAGAAGATCCGTTTACAAACCAACACTTGGACCAACGCTACTTGTCTGCTTTCGAAGAC 660
DB 201 ProGluGlySerGlyTyAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220
QY 661 TCTGAATAGGTGACGAGTGAAGCTAACTTCACTGCTTGTTCGCTCCAGCTATTAGA 720
DB 221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
QY 721 GCTAGATTGGAAGTGAAGTCCAGGTTTACTTGTGACTGACGAAGAGCTGTTCATCTG 780
DB 241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyLeu 260
QY 781 ATGGACATGTGTCCATTCGACACTGTCGCTAGAACTTCTGACGCTACTGAATGTCTCCA 840
DB 261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280
QY 841 TTCGTGCTTGTGTTTCACTCAGCAGCAATGATGATCAATACGACTACTTTCGAAAGCTTGGGT 900
DB 281 PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyAspTyLeuGlnSerLeuGly 300
QY 901 AAGTACTACGGTTACGGTGTGGTAAACCATTTGGTCCAGCTCAAGCTGTGTGGTTTCGCT 960
DB 301 LysTyTyGlyTyGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320
QY 961 AACGAATGTATGCTAGATTGCTCACTCTCCAGTTCAGACCAACACTTCTTACTTAACCAAC 1020
DB 321 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis 340

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QY 1081 CACGACACACTATGATATCTATTTCTTCGCTTTGGGTTTGTACAAACGGTACCAAGCCA 1140
DB 361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyAsnGlyThrAlaPro 380
QY 1141 TTGCTACTACTTCTGTTCAATCTATIGAGAAACTGACGGTTACICIGCTTCTTGGACT 1200
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QY 1201 GTTCCATTCGCTGCTAGAGCTTACGTTGAAATGATGCAATGTCAAGCTCAAAAGAAACCA 1260
DB 401 ValProPheGlyAlaArgAlaTyValGluMetMetGlnCysGlnAlaGluLysGluPro 420
QY 1261 TTGGTTAGAGTTTGGTTAACGACAGAGTTGTCCATTCGACGGTGTGCTGTTGCACAG 1320
DB 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440
QY 1321 TTGGGTAGATGTAACGACAGACGACTCGTIGAAGTTTGTCTTTCGCTAGATCTGGTGGT 1380
DB 441 LeuGlyArgCysLysArgAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGCTGCAATGTTTCGCT 1401
DB 461 AsnTrpAlaGluCysPheAla 467

RESULT 2
US-09-121-425-1
; Sequence 1, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: Consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121,425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-121-425-1

Alignment Scores:
Pred. No.: 1-75e-223 Length: 441
Score: 2282.00 Matches: 431
Percent Similarity: 98.41% Conservative: 3
Best Local Similarity: 97.73% Mismatches: 7
Query Match: 92.02% Indels: 0
DB: 3 Gaps: 0

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QY 139 TTGTGGGGTACCTACTCTCCATCTTCTTGGCAGACGAATCTGCTATTCTTCCAGAC 198
DB 21 LeuTrpGlyGlnTySerProTyPheSerLeuGluAspGluSerAlaIleSerProAsp 40
QY 199 GTTCCAGACGACTGTAGACTTACTTCTCGTTCAGTTTTCCTAGACACGGTCTAGATAC 258
DB 41 ValProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyAlaArgTy 60
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QY 319 ACTGCTTTCACGGCTAAGTACGCTTCTTGAAGACTTACAACTACACACTTGGTCTGCAC 378
Db 81 ThrAlaPheLysGlyLysTyrAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAsp 100
QY 379 GACTTGACTCCATTCGGTGAACCAACAAATGGTTAACTCTGGTATTAAAGTTCTACAGAGA 438
Db 101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyIleLysPheTyrArgArg 120
QY 439 TACAAGCCTTTCGGTAGAAGATGTTCCATTCATAGAGCTTCTGGTCTGCACAGAGTT 498
Db 121 TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal 140
QY 499 ATTGCTTCTCGCTGAAGTTTCATGAAGTTTCCAACTGCTAAAGTTGGCTGACCCAGGT 558
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QY 559 TCTAACCCACACAGCTTCTCCAGTTATTACGTGATCATTCACAGAGGATCCGGTTAC 618
Db 161 SerGlnProHisGlnAlaSerProValIleAspValIleIleProGlyGlySerGlyTyr 180
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QY 679 GTTGAAGCTTAACCTACACTGCTTTGTTGCTCCAGCTATTAGAGCTAGATTGGAAGCTGAC 738
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QY 919 GCTGTAACCCATTGGTCCAGCTCAAGCTGTGTTTCGCTAAAGAAATTTGATGCTAGA 978
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QY 1039 GCTACTTTCCTTGAACGCTACTTTGTACGTGACTTCTTCACAGACACAACTAIGATA 1098
Db 321 AlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnSerMetIle 340
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Db 441 Ala 441
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US-09-634-493A-1
: Sequence 1, Application US/09634493A
: Patent No. 6579975
: GENERAL INFORMATION:
: APPLICANT: Lehmann, Martin
: TITLE OF INVENTION: Consensus Phytases
: FILE REFERENCE: consensus phytases 13239
: CURRENT APPLICATION NUMBER: US/09/634.493A
: PRIOR FILING DATE: 2000-08-08
: PRIOR APPLICATION NUMBER: US/09/121.425
: PRIOR FILING DATE: 1998-07-23
: PRIOR APPLICATION NUMBER: EPO 97112688.3
: PRIOR FILING DATE: 1997-07-24
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 441
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: consensus
: OTHER INFORMATION: sequence
US-09-634-493A-1
Alignment Scores:
Pred. No.: 1,75e-223 Length: 441
Score: 2282.00 Matches: 431
Percent Similarity: 98.41% Conservative: 3
Best Local Similarity: 97.73% Mismatches: 7
Query Match: 92.02% Indels: 0
DB: 4 Gaps: 0
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QY 199 GTTCCAGACGACTGTAGAGTTACTTTCGTTCAAGTTTGTCTAGACACGGTGTAGATAC 258
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QY 259 CCAACTTCTCTGCTCTAAGGCTTACTCTGCTTGTGATGAGCTATTCAAAAGAACGCT 318
Db 61 ProThrSerSerLysSerLysAlaTyrSerAlaLeuIleGluAlaIleGlnLysAsnAla 80
QY 319 ACTGCTTTCACGGTGAAGTACGCTTCTTGAAGACTTACAACTACACACTTGGTCTGCAC 378
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QY 379 GACTTGACTCCATTCGGTGAACCAACAAATGGTTAACTCTGGTATTAAAGTTCTACAGAGA 438
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Db 161 SerGlnProHisGlnAlaSerProValIleAspValIlelleProGluGlySerGlyTyr 180
QY 619 AACAAACACTTGGACCAAGCTTCTGACTGCTTTCGAAGACTCTGAATTAGTGTGAC 678
Db 181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200
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QY 919 GCTGGTAAACCAATGGGTCCAGCTCAAGGTGTGGTTCGCTCAACGAATGATGTCTAGA 978
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Db 441 Ala 441

RESULT 4

US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/121.425
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3

; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-09-121-425-2

Alignment Scores:
Pred. No.: 3,03e-222 Length: 467
Score: 2270.00 Matches: 437
Percent Similarity: 90.35% Conservative: 3
Best Local Similarity: 89.73% Mismatches: 7
Query Match: 91.53% Indels: 40
DB: 3 Gaps: 2
US-09-488-265b-28 (1-1404) x US-09-121-425-2 (1-467)

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QY 241 AGACAGGTGTAGATACCAACTTCTCTCGCTCTAAGGCTTACTCTCTTGTATTGAA 300
Db 81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla ----- 97
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Db 181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200
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QY 1081 CACGACAACTATGATATCTATTTCTTCGCTTTGGGTTCGTACAAGGTACCAAGCCA 1140
DB 361 HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro 380
QY 1141 TGTCTACTACTCTGTTGCACTATTTGAGAACTGACGGTTACTCTGCTTCTGGACT 1200
DB 381 LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThr 400
QY 1201 GTTCCATTGCTGCTAGAGCTTACGTTGAATGATGCAATGTCAGCTGAAAGGAGCCA 1260
DB 401 ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGlnPro 420
QY 1261 TTGGTTAGAGTTTGGTTAACGACAGAGTTGTCCATTTGCACGGTTGCTGTTGACAA 1320
DB 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValAspLys 440
QY 1321 TTGGGTAGATGTAAGAGACGACTCTGGTTGAAGGTTTCTCTTCGCTAGACTCTGGTGT 1380
DB 441 LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGCTGAATGTTTCGCT 1401
DB 461 AsnTrpAlaGluCysPheAla 467

RESULT 5

US-09-634-493A-2
; Sequence 2, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; TITLE OF INVENTION: Consensus Phytases
; FILE REFERENCE: Consensus phytases 13239
; CURRENT APPLICATION NUMBER: US/09/634,493A
; CURRENT FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121,425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-634-493A-2

Alignment Scores:
Prod. No.: 3,03e-222 Length: 467
Score: 2270.00 Matches: 437
Percent Similarity: 90.35% Conservative: 3
Best Local Similarity: 89.73% Mismatches: 7
Query Match: 91.53% Indels: 40
Gaps: 2
US-09-488-265B-28 (1-1404) x US-09-634-493A-2 (1-467)
QY 1 ATGGCGCTGTTTCGCTGCTACTCTCCATTGCCACCTTGTTCGGTTCACATCCGGTACC 60
DB 1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20
QY 61 GCCTGGGCTCCTCGTGGTAATCTTCACCTCTGTCTGACACAGTGTGACGGTGGTTACCAATGT 120
DB 21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40
QY 121 TTCCAGAAATTTCTCACTTGTGGGTACCTACTCTCCATACCTCTCTCTTTGGCAGACGAA 180
DB 41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60
QY 181 TCTGCTATTTCTCCAGAGCTTCCAGACACTGTAGAGTTACTTTCGTTCAAGTTTGTCT 240
DB 61 SerAlaIleSerProAspValProAspAspCysArgValThrPheValGlnValLeuSer 80
QY 241 AGACACGGTGTAGATACCCAACTTCTTCTCGCTAAGGCTTACTCTCTGCTTTCATTCAA 300
DB 81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla 97
QY 301 GCTATTCAAAAGAAGCGCTACTGCTTTCAAAGGTAACTACGCTTTCCTGAAGACTTCAAC 360
DB 98 -----ThrTyrAsn 100
QY 361 TACACTTTGGTGGTGGACGACTTGCACGCCATTCGCTGAAACCAATGTTAACTCTGGT 420
DB 161 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120
QY 421 ATTAAGTTCTACAGAGATACAAGCTTTGGCTAGAAAGATGTTCACATTCATTAGACCT 480
DB 121 IleLysPheTyrAlaArgGlyLysAlaLeuAlaArgLysIleValProPheIleArgAla 140
QY 481 TCTGTTCTGACAGAGTTATGCTTCTGCTGAAAGTTTCATTGAAGGTTTCCAACTCTGCT 540
DB 141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160
QY 541 AAGTTGGCTGACCCAGGTTCTCAACCCACCAAGCTTCTCCAGTTTATTAAC----- 591
DB 161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180
QY 592 -----GTGATCAT 600
DB 181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200
QY 601 CCAGAAGGATCCGGTTACAAACAACACTTTGGACCCAGGTACTTGTACTGCTTTCGAAGAC 660
DB 201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220
QY 661 TCTGAATTAGGTGACGAGCTTGAAGCTAACTTCACIGCTTTGTTGCTCCAGCTATTAGA 720
DB 221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
QY 721 GCTAGATTGGAAGCTGACTTCCAGGCTTACTTTGACTGACGAAGAGGTTGTTTACTTG 780
DB 241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260
QY 781 ATGGACATGTGCTCATTCGACACTGCTCGCTAGAACTTCTGACGCTACTGAATGTCTCCA 840
DB 261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro 280
QY 841 TTCTGTGCTTTTTCACCTCACGACGAATGGATGCCAATACGACTACTTCCAAAGCTTGGGT 900
DB -----

281	Db	PhcCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly	300
901	Qy	AACTACTACGGTTACGGTGCTGGTAACCCATTGGGTCCAGCTCAAGGTGTGGTTTCGGT	960
301	Db	LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla	320
961	Qy	AACGAATTGATGCTAGATGACTACTCTCCAGTTTCAAGACACACTTCTTACTATACCAC	1020
321	Db	AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis	340
1021	Qy	ACTTTGGACTCTAACCCAGCTACTTTCCCATTCGAACGCTACTTTGACCGCTGACTCTCT	1080
341	Db	ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer	360
1081	Qy	CAGGACAACACTATGATATCTATTCTTCGCTTGGGTTGTACAACTGATACAGCCCA	1140
361	Db	HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaPro	380
1141	Qy	TTGCTCTACTCTCTGTGTAATCTATTGAAAGAACTGACGGTACTCTGCTCTTGGCACT	1200
381	Db	LeuSerThrThrSerValGluSerIleGluGlnThrAspGlyTyrSerAlaSerTTPhr	400
1201	Qy	GTTCCATTCCTCGTAGAGCTTACGTTGAATGATSCAATGTCAAGCTGAAGGAAACCA	1260
401	Db	ValProPheGlyAlaArgAlaTyrValGluMetGlnCysGlnAlaGluLysGluPro	420
1261	Qy	TTGGTTAGAGTTTGGTTTAACGACACAGAGTTGTTCCTATTGCACGGTGTGCTGTGTACAAG	1320
421	Db	LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysAlaValaspLys	440
1321	Qy	TTGGGTAGATGTTAAGACAGACGACTCTGGTTGAAGGTTTGTCTTTCGCTAGACTGTGGGT	1380
441	Db	LeuGlyArgCysLysArgAspPheValGluGlyLeuSerPheAlaArgSerGlyGly	460
1381	Qy	AACTGGGCTGAAATGTTTCGCT	1401
461	Db	AsnTirAlaGluCysPheAla	457

RESULT 6

US-07-923-724-8
 ; Sequence 8, Application US/07923724
 ; Patent No. 5780292
 ; GENERAL INFORMATION:
 ; APPLICANT: Nevalainen, Helena K. M.
 ; APPLICANT: Paloheimo, Marja T.
 ; APPLICANT: Miettinen-Oinonen, Aija S.K.
 ; APPLICANT: Torkkeli, Tuula K.
 ; APPLICANT: Cantrell, Michael
 ; APPLICANT: Piddington, Christopher S.
 ; APPLICANT: Rambosk, John A.
 ; APPLICANT: Turunen, Maria K.
 ; APPLICANT: Fagerstr m, Richard B.
 ; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
 ; TITLE OF INVENTION: In Trichoderma
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 ; STREET: 1100 New York Avenue, Suite 600
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/923,724
 ; FILING DATE: 31 JUL-1992
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/496,155

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Db 201 SerGluAlaSerSerAsnThrLeuAspProGlyThrCysThrVal-PheGluAsp 220
Qy 661 TCTGAATTAGTGGAGGCTTGAGCTTAACCTTCTACTGCTTTGCTGCTCCAGCTATTAGA 720
Db 221 SerGluLeuAlaAspThrValGluAlaAsnPheThrPheAlaProSerIleArg 240
Qy 721 GCTAGATTGGAGCTGACTTCCAGGCTTACTTTGACTGACGAGAGCTGTTTACTTG 780
Db 241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260
Qy 781 ATGGACATGTCTCCATTCGACACCTGCTGAGACTTCTGAGCTTCTGAGCTACTGAAATCTCCCA 840
Db 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
Qy 841 TCTGCTGCTTGTTCACCTACGACGAGATGGATGATCAATACGACTACTTCCAAAGCTTGGT 900
Db 281 PheCysAspLeuPheThrHisAspGluTrpIleHisTyrAspThrLeuGlnSerLeuLys 300
Qy 901 AAGTACTACGGTTACGGTGTGGTAAACCCATTGGGTCACGCTCAAGGTGTGGTTCGCT 960
Db 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
Qy 961 AAGCAATGATTGCTAGATTGACTACCTCTCCAGTTTCAAGACCACACTTCTACTATAAC 1020
Db 321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 1040
Qy 1021 ACTTGGACTCTAACCCAGCTACTTCCCATTTGACGCTACTTCTACGCTGAGCTTCT 1080
Db 341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360
Qy 1081 CACGACAACTATGATACTATTCTTCTGCTTTGGGTTTGTACAGGTTACCAAGCCA 1140
Db 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuIleAsnGlyThrLysPro 380
Qy 1141 TTGCTACTACTTCTGTTGATCTATTCGAAAGAACTGACGGTTACTGCTTCTTGGACT 1200
Db 381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaIleThr 400
Qy 1201 GTTCTCATTCGCTGCTAGAGCTTACGTTCAATGATGAATGTCAGGTCGAAAGCAACCA 1260
Db 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGlyPro 420
Qy 1261 TTGCTAGAGTTTGGTTTAACACAGAGTGTCTCCATTGACGCTGTGCTGTGACAAG 1320
Db 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProIleAspAla 440
Qy 1321 TTGGGTAGCACTAAGACAGACGACTTGGTTCAAGGTTTGTCTTTCGCTAGATCTGGTGGT 1380
Db 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
Qy 1381 AACTGGGCTGAATGTTTCGCT 1401
Db 461 AspTrpAlaGluCysSerAla 467
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RESULT 7

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US-08-609-426A-8
; Sequence 8, Application: US/08609426A
; Patent No. 5830733
; GENERAL INFORMATION:
; APPLICANT: Nevalainen, Helena K.M.
; APPLICANT: Paloheimo, Marja T.
; APPLICANT: Miettinen-Oinonen, Arja S.K.
; APPLICANT: Torkkeli, Tuula K.
; APPLICANT: Cantrell, Michael
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Rambosk, John A.
; APPLICANT: Turunen, Marja K.
; APPLICANT: Fagerström, Richard B.
; APPLICANT: Houston, Christine S.
; TITLE OF INVENTION: Production of Phytase Degrading Enzymes
; TITLE OF INVENTION: in Trichoderma
; NUMBER OF SEQUENCES: 69
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1100 New York Avenue, Suite 600
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,426A
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/923,724
; FILING DATE: 31-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/496,155
; FILING DATE: 19-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/044,077
; FILING DATE: 29-APR-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: UK 8610600
; FILING DATE: 30-APR-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Reed, Grant E.
; REGISTRATION NUMBER: P-41,264
; REFERENCE/DOCKET NUMBER: 1050, 0080001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-609-426A-8
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Alignment Scores:
Pred. No.: 1-93e-182 Length: 467
Score: 1879.00 Matches: 353
Percent Similarity: 84.37% Conservative: 41
Best Local Similarity: 75.59% Mismatches: 73
Query Match: 75.77% Indels: 0
DB: 2 Gaps: 0
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CS-09-488-265B-28 (1-1404) x US-08-609-426A-8 (1-467)

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Qy 1 ATGGGGGTGTTGCTGCTGCTACTGTCCATTGCCACCTTGTTCGGTTCACATCCGGTACC 60
Db 1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuAlaGlyValThrSerGlyLeu 20
Qy 61 GCCTGGGCTCCTGGTGAATTCCTACTCTGTGACACTGTGTGACGCTGGTTACCAATGT 120
Db 21 AlaValProAlaSerArgAsnGlnSerThrCysAspThrValAspGlnGlyThrGlnCys 40
Qy 121 TTCACAGAAATTTCTCAGTTGTGGGTACTCTCTCCATACITCTCTTTGGCAGACGAA 180
Db 41 PheSerGluThrSerHisLeuTyrGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60
Qy 181 TCTGCTATTTCTCCACAGCTTCCAGACGACTGTAGAGTTACTTCTGCTCAAGTTTGTCT 240
Db 61 SerAlaIleSerProAspValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80
Qy 241 AGACACGGTGTAGATACCACTTCTTCTGCGTCTTAAGGCTTACTCTGCTTGTATTGAA 300
Db 81 ArgHisGlyAlaArgTyrProThrGluSerLysGlyLysLysTyrSerAlaLeuIleGlu 100
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[illegible]

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Db          461 AsptirPa.glucySserAla 467
RESULT #
US-06-374-652C-2
: Sequence 2, Application US/08374652C
: Patent No. 5834286
: GENERAL INFORMATION:
: APPLICANT: NEVALAINEN, HELENA K.M.
: APPLICANT: PALOHEIMO, MARJA T.
: APPLICANT: FAGERSTROM, RICHARD B.
: APPLICANT: MATTINEN-OINONEN, ARJA S.
: APPLICANT: TURUNEN, MARJA K.
: APPLICANT: RAMBOSEK, JOHN A.
: APPLICANT: PIDDINGTON, CHRISTOPHER S.
: APPLICANT: HOUSTON, CHRISTINE S.
: APPLICANT: CANTRELL, MICHAEL A.
: TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
: TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING
: TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
: NUMBER OF SEQUENCES: 94
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
: STREET: 1100 NEW YORK AVENUE, SUITE 600
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: F-oppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/374,652C
: FILING DATE: 24-MAY-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/US93/07058
: FILING DATE: 27-JUL-1993
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/925,401
: FILING DATE: 31-JUL-1992
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: REED, GRANT E.
: REGISTRATION NUMBER: 41,264
: REFERENCE/DOCKET NUMBER: 1050.071061
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-371-2600
: TELEFAX: 202-371-2540
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 467 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: not relevant
: MOLECULE TYPE: protein
US-08-374-652C-2
Alignment Scores:
Pred. No.: 1-930-182 Length: 467
Score: 1879.00 Matches: 353
Percent Similarity: 84.37% Conservative: 41
Best Local Similarity: 75.59% Mismatches: 73
Query Match: 75.77% Indels: 0
DB: 2 Gaps: 0

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Db 1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuAlaGlyValThrSerGlyLeu 20
QY 61 GCCTTGGGTCCTCGTGGTAATCTCTACTCTTGACACATGTTGACGGTGGTTACCAATST 120
DB 21 AlaValProAlaSerArgAsnGlnSerThrCysAspThrValAspGlnGlyTyrGlnCys 40
QY 121 TCCCAAGAAATTCACATCTGGGGTACCTACTCTCCATACCTCTCTCTTTGGCAGACGAA 180
DB 41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60
QY 181 TCTGCTATTCCTCCACAGCTTCACAGAGCTCTAGAGTTCATCTTCCTCAAGCTTTGTCT 240
DB 61 SerAlaIleSerProaspValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 50
QY 241 AGACAGGTCGTAGATACCAACTCTCTCGGCTTAAGGCTTACTCTGCTTTGATTCGA 300
DB 81 ArgHisGlyAlaArgTyrProThrGluSerLysGlyLysTyrSerAlaLeuIleGlu 100
QY 301 GCTATTCAAGAAGCGCTACTGCTTCTCAAGGCTAAGTACGCTTCTTGAAGACTTACAAC 360
DB 101 GluIleGlnGlnAsnValThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 361 TACACTTGGGTCCTCAGCAGCTTACTCCATTCGGTGAAGCAAACTGTTAACTCTGT 420
DB 121 TyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 421 ATTAGTTCACAGAGATACAGGCTTGGGTAGAAAGATTTGCCATTTCATTAGACT 480
DB 141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleGlnProPheIleArgSer 160
QY 481 TCTGGTTCGACAGACTTATTCCTCTGCTGAAAGTTCATTAAGGTTTCCAACTCTCT 540
DB 161 SerGlySerSerArgValIleAlaSerGlyGluLysPheIleGlyPheGlnSerThr 180
QY 541 AGTTGGCTGACCCAGGTTCTCAACACACAGCTTCTCCAGTATTAACTGATCAT 600
DB 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValValIle 200
QY 601 CCAGAGGATCCGGTACACACACACTTTGGACCAGGTTACTGTACTGCTTCCAGAC 560
DB 201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY 661 TCTGAATTAGTGACGAGCTTAAGCTTAACCTCCTGCTTCTCCCTCCAGCTATTAGA 720
DB 221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheAlaProSerIleArg 240
QY 721 GCTAGATTGGAAGCTACTGTCGAGGTGTACTTTGACTGACGAGACAGCTGTTTACTTG 780
DB 241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260
QY 781 ATGCAGATGTCTCATTGACACTGTCGCTAGAACTTCTGACGCTACTCAATGTCTCCA 840
DB 261 MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
QY 841 TTCCTGCTTGTTCACCTCACGAGAAATGATCCAAATAGCACTACTTGCAAAGCTTGGT 900
DB 281 PheCysAspLeuPheThrHisAspGluTyrIleHisTyrAspTyrLeuGlnSerLeuLys 300
QY 901 AAGTACTACGGTTACGGTGTGTGTACCCATTCGGTCCAGCTCAAGGTGTGTTTCCGT 960
DB 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
QY 961 AACGAATTGATTCCTAGATTGACTCACTCTCCAGTTCAAGACCACACACTTCTACTACCA 1020
DB 321 AsnGluLeuIleAlaArgIleuThrHisSerProValHisAspAspThrSerSerAsnHis 340
QY 1021 ACTTTGCACTTAACCCAGCTACTTTCCCAITGACGCTACTTTGTACGCTGACTTCTCT 1080
DB 341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360
QY 1081 CAGCACAACTATGATATCTATTCTCTCGCTTGGGTTGTACACGGTACCAAGCCA 1140
DB 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380

QY 1141 TTGTCTACTACTTCTGTGTGAATCTATTGAAGAACTGACCGTACTTCTGCTTCTTGGACT 1200
DB 381 LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTrpThr 400
QY 1201 GTTCCATTGCGTCTAGAGCTTACGTTGAATGATCAATGCTCAAGCTGAAAGGAACCA 1260
DB 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro 420
QY 1261 TTGTTAGAGTTTGGTTAAGCAGAGAGTGTTCCTATTGACGCTTGTGCTGTTGACAAG 1320
DB 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProIleAspAla 440
QY 1321 TTGGTAGATCTAGAGAGAGAGCTTCTGTTGAAGGTTTGCTTTTCGTAGATCTGTTGCT 1380
DB 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGCTGAATGTTCCGT 1401
DB 461 AspTrpAlaGluCysSerAla 457
RESULT 9
US-08-151-574-32
: Sequence 32, Application US/08151574
: Patent No. 5436156
: GENERAL INFORMATION:
: APPLICANT: Robert F.M. Van Gorkom
: APPLICANT: Willem Van Hartingsveldt
: APPLICANT: Petrus A. Van Paridon
: APPLICANT: Annemarie E. Veenstra
: APPLICANT: Rudolf G.M. Luttin
: APPLICANT: Gerardus Sellen
: TITLE OF INVENTION: Cloning and Expression of Microbial
: TITLE OF INVENTION: Phytase
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
: ADDRESS: Morrison & Focrster
: STREET: 545 Middlefield Road, Suite 200
: CITY: Menlo Park
: STATE: California
: COUNTRY: USA
: ZIP: 94025-3471
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: SOFTWARE:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/151,574
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 07/688,578
: FILING DATE: 24-MAY-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: Murashige, Kate H.
: REGISTRATION NUMBER: 29,959
: REFERENCE/DOCKET NUMBER: 24615-20026.00
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-327-7250
: INFORMATION FOR SEQ ID NO: 32:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 467 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-151-574-32
Alignment Scores:
Pred. No.: 4,93e-182 Length: 467
Score: 1875.00 Matches: 353
Percent Similarity: 84.37% Conservative: 41

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Best Local Similarity: 75.59%      Mismatches: 73
Query Match: 75.60%              Indels: 0
DB: 1                             Gaps: 0
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US-09-488-265B-28 (1-1404) x US-08-151-574-32 (1-467)

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DB	1	MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu	20
QY	61	GCCTTGGGTCCTGGTGAATCTTCACICTCTGTGACACTGTTCACGCGTGGTACCACATGT	220
DB	21	AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys	40
QY	121	TTCGAGAAATTTCTCAGTCTGGGTACTACTCTCCATACTCTCTTTGGCAGACAGAA	180
DB	41	PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu	60
QY	181	TCGTCTATTCTCCAGACGTTCCAGACGACTGAGAGTACTTCCTCAAGTTTGTTCT	240
DB	61	SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer	80
QY	241	AGACAGGTCCTAGATACCCAACTCTCTCGCCGCTTAAGCGTTACTCTCTCTGATTGAA	300
DB	81	ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleGlu	100
QY	301	GCTATTCAAAGAAGCGTACTCGCTTTCAAGGGTAAGTACGCTTTCTTGAAGACTTACAAC	360
DB	101	GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn	120
QY	361	TACACTTTGGTGGCTGACGACTTGACTCCATTTCGGTGGAACCAAAATGGTTACTCIGGT	420
DB	121	TyrSerLeuGlyAlaAspSerLeuThrProPheGlyGluGlnLeuValAsnSerGly	140
QY	421	ATTAAAGTCTCACAGAAGATCAAGGCTTTGGCTAGAAAGATGTTCATTTCATTAGAGCT	480
DB	141	IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer	160
QY	481	TCGTGGTCTGACAGAGTTATGCTTCGTGTGAAGATTCATTGAAGGTTTCCAACTCGT	540
DB	161	SerGlySerSerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr	180
QY	541	AAGTTGCTCACCACGAGTTCTCAACACACACCAAGCTTCTCCAGTTATTACAGTGATCATI	600
DB	181	LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValIle	200
QY	601	CCAGAAGGATCCGGTTACACACACACTTTGGACACACGCTACTTGCTGCTTCCGAAGAC	660
DB	201	SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp	220
QY	661	TCGTGAATTAGTACACGAGTTGAAGCTTAACCTTCACICTGTTTGTTCGCTCCACGCTATTAGA	720
DB	221	SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg	240
QY	721	GCTAGATTGGAAGCTGACTTCGCAGGTGTACTTTGACTACGACAGACGTTGTTTACTTG	780
DB	241	GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGlnGlyValThrTyrLeu	260
QY	781	ATGCACATGTTCGCAITTCGACACTGTGCGTAGAACTTCTCAGCGTCACTGAATTCGTCCA	840
DB	261	MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro	280
QY	841	TTCTGTGCTTTGTTCATCAGCAGGAATGGATCCAAATACGACTACTTTCGAAAGCTTGGGT	900
DB	281	PheCysAspLeuPheThrHisAspGlyTrpIleAsnTyrAspTyrIleuGlnSerLeuLys	300
QY	901	AAGTACTACGGTTACGGTGGTGAACCCATTGGTGCCAGCTCAAGGTGTGGTTTCGCT	960
DB	301	LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla	320
QY	961	AACGAATTGATTGCTAGATTGACTCACTCTCCAGTCTTCAGACACACACTTCTACTAACCAC	1020
DB	321	AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspThrSerSerAsnHis	340

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/419,448
FILING DATE: 10-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-1500
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-419-448-32

Alignment Scores:
Pred. No.: 4,93e-182 Length: 467
Score: 1875.00 Matches: 353
Percent Similarity: 84.37% Conservativity: 41
Best Local Similarity: 75.59% Mismatches: 73
Query Match: 75.60% Indels: 0
DB: 2 Gaps: 0

US-09-488-265B-28 (1-1404) x US-08-419-448-32 (1-467)

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QY 1 ATGGCGGTGTCGTCGTACTGTCATTCACATTCGACACTGTCGTCACATTCGCGTTCACATTCGCGTACC 60
DB 1 MetGlyValSerAlaValLeuProLeuTyrLeuSerGlyValThrSerGlyLeu: 20

QY 61 GCCTTGGTCTCGTGGTAATCTCCTGACACTGTCGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 120
DB 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40

QY 121 TTCACGAAATTCACATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 180
DB 41 PheSerGluThrSerHisLeuTyrGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60

QY 181 TCCTGCTATTCCTCCAGACGTCCTGACGACGTCCTGACGTCCTGACGTCCTGACGTCCTGACGTCCTGCT 240
DB 61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80

QY 241 AGACAGGTCGTAGATACCAACTCTCTCTGCGTCCTAAGGTCCTAAGGTCCTAAGGTCCTAAGGTCCTAAG 300
DB 81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysLysLysLysLysLysLysLysLysLys 100

QY 301 GCTATTCAAACGCTACTCTCTCAAGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 360
DB 101 GluLeuGlnGlnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120

QY 361 FACACTTTGGTGGTCGACGACGTCCTGACGTCCTGACGTCCTGACGTCCTGACGTCCTGACGTCCTGACGTC 420
DB 121 TyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140

QY 421 ATTAAGTCTACAGAGATACAAAGCTTTGGTCGTAGAAAGATTTCCATTCATTCATTCATTCATTCATTCAT 480
DB 141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160

QY 481 TCTGGTCTCAGACGCTATTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 161 SerGlySerSerArgValIleAlaSerGlyLysLysLysLysLysLysLysLysLysLysLysLysLys 180

QY 541 AAGTGGTGGTCGACGCTCTCAACACACACGTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 600
DB 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerProLysIleAspValIle 200

QY 601 CCAGAGGATCCGGTTACAAACACACTTTGGACCGGTCCTTGGACCGGTCCTTGGACCGGTCCTTGGACGAC 660
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
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20 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY 661 TCTGAATTAGTACGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCTGACGCT 720
DB 221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
QY 721 GCTAGATTGGAAGCTGACTTGCAGGTTGTTACTTGTACCTGACGAGGAGGTCGTTGTTGTTGTTGTTGTTG 780
DB 241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260
QY 781 ATGACATGTGTCATTCGACACTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 840
DB 261 MetAspMetCysSerPheAspThrIleSerThrValAspThrValAspThrLysLeuSerPro 280
QY 841 TCTGTGCTTGTTCACCTCAGGACGATGATCCATACGACGTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTC 900
DB 281 PheCysAspLeuPheThrHisAspGluTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300
QY 901 AAGTACTACGCTTACGCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 960
DB 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
QY 961 AACGAATGATGCTAGATGACGTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1020
DB 321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340
QY 1021 ACITGGACTCTAACCCAGCTACTTCCCATTTGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1080
DB 341 ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360
QY 1081 CACGACACACTATGATATCTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
DB 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380
QY 1141 TTGCTACTACTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1200
DB 391 LeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaIleThr 400
QY 1201 GTTCATTGCTGCTAGAGCTTACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1260
DB 401 ValProPheAlaSerArgLeuTyrValGluMetGlnCysGlnAlaGluGlnGluPro 420
QY 1261 TTGCTAGATTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1320
DB 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440
QY 1321 TTGGTGTAGTACAGAGGACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1380
DB 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGCTGAATGTTTCGCT 1401
DB 461 AspTrpAlaGluCysPheAla 467
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RESULT 13

US-08-819-825-3
Sequence 3, Application US/08819825
Patent No. 5866118
GENERAL INFORMATION:
APPLICANT: Berk, Randy M.
APPLICANT: Ray, Michael W.
APPLICANT: Klotz, Alan V.
TITLE OF INVENTION: Polypeptides Having Phytase Activity
TITLE OF INVENTION: And Nucleic Acids Encoding Same
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: No. 58661180 No. 5866118disk of No. 5866118th America, Inc.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10174-6401
COMPUTER READABLE FORM:

Cy	601	CGAAGAGATCCGGTTACACACACACTTTCGACACACGCTACTGTACTGCTTCTCGAAGAC	660
Lb	201	SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp	220
Cy	661	TCGCAATTAGGTGACGACGCTTGAAGCTAACTTCACCTCTTGTCGCTCCAGCTATTAGA	720
Lb	221	SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg	240
Cy	721	GCTAGATTGGAAGCTGACTTCGCCAGGTGTTACTTTGACTGACGAAGACGTTGTACTTG	780
Lb	241	GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu	260
Cy	781	ATGCACATGTGTCATTTCGACACTGTCGCTAGACACTTCTCAGCGCTACTGAATTCGICCCA	840
Lb	261	MetAspMetCysSerPheAspThrIleSerThrValAspThrIleAspThrLeuSerPro	280
Cy	841	TTCTGTGCTTGTTCACATCAGCAGCAATGATCCCAATACGACTACTTCGAAAGCTGGG	900
Lb	281	PheCysAspLeuPheThrHisAspGluTyrIleAsnTyrAspTyrLeuGlnSerLeuLys	300
Cy	901	AAGTACTACGGTTACGGTGTGTTAACCCATTTGGTCCAGCTCAAGGTGTGTTTCGCT	960
Lb	301	LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla	320
Cy	961	AACGAATTGATTGCTACGATTGACTCACTCTCCAGTTCACAGCACCACACTTCTACTAAC	1020
Lb	321	AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis	340
Cy	1021	ACTTTGAGCTCTAACCCAGCTACTTTCCCATTTGAACGCTACTTTGTACGCTGACTTCT	1080
Lb	341	ThrLeuAspSerSerProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer	360
Cy	1081	CACCACAACTATGATATCTATTCTTCGCTTGGTTGTACAACGGTACCAAGCCA	1140
Lb	361	HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro	380
Cy	1141	TTGTCTACTACTCTGTGTGAATCTATTGACAGAACTGACGTTTACTCTGCTTCTTGGACT	1200
Lb	381	LeuSerThrThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyrThr	400
Cy	1201	GTTCCATTTCGCTGCTAGAGCTTACGTTGAATGATGCAATGTCACGCTGAANAGGAACCA	1260
Lb	401	ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnGluPro	420
Cy	1261	TTGGTTAGAGTTTGGTTAACGACAGAGTGTTCCTCATTCGACGTTGTGCTGTGACAAAG	1320
Lb	421	LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla	440
Cy	1321	TTGGGTAGATGCTAAGAGACGACGACTTCGTTCAAGGTTGTCTTCGCTAGATCTGGTGGT	1380
Lb	441	LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly	460
Cy	1381	AACTGGGCTGAATGTTTCGCT 1401	
Lb	461	AspThrAlaGluCysPheAla 467	

RESULT 14
 US-09-163-642-3
 ; Sequence 3, Application US/09163642
 ; Patent No. 6221644
 ; GENERAL INFORMATION:
 ; APPLICANT: Berka, Randy M.
 ; APPLICANT: Ray, Michael W.
 ; APPLICANT: Klotz, Alan V.
 ; TITLE OF INVENTION: Polypeptides Having Phytase Activity
 ; TITLE OF INVENTION: And Nucleic Acids Encoding Same
 ; NUMBER OF SEQUENCES: 5
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: No. 62216440 No. 6221644disk of No. 6221644th America, Inc.
 ; STREET: 405 Lexington Avenue, Suite 6400
 ; City: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.

ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA: US/09/163,642
APPLICATION NUMBER: US/09/163,642
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/819,825
FILING DATE: 18-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Landiris, Elias J.
REGISTRATION NUMBER: 33,728
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 867 0123
TELEFAX: 212 867 0298
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-163-642-3

Alignment Scores:
Pred. No.: 4,33e-182 Length: 467
Score: 1875.00 Matches: 353
Percent Similarity: 84.37% Conservative: 41
Best Local Similarity: 75.59% Mismatches: 73
Query Match: 75.60% Indels: 0
DB: 3 Gaps: 0

US-09-488-265B-28 (1-1404) x US-09-163-642-3 (1-467)

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QY 1 ATGGCGTGTCGTGCTGCTACTGTCCATTCACCTGTCGTGTCACCTGTCACCTCCCGTACC 60
DB 1 MetGlyValSerAlaValLeuLeuProLeuTyLeuSerGlyValThrSerGlyLeu 20
QY 61 GCCTTGGTGCTCGTGTAATCTCACTCTGTGACACTGTGTGACGGTGGTACCAATCT 120
DB 21 AlaValProAlaSerArgAsnGlnSerSerCysAspThrValAspGlnGlyTyrGlnCys 40
QY 121 TTCACCAAAATTCCTCACTTGTGGGTACCTACTCTCCATCTCTCTTTGTCAGACGAA 180
DB 41 PheSerGluThrSerHisLeuTyrPheGlyGlnTyrAlaProPhePheSerLeuAlaAsnGlu 60
QY 161 TCIGCTATTCTCCAGACGCTCCAGACGACTGTAGAGTTACTTTCGTTCCAGTTTGTCT 240
DB 61 SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80
QY 241 AGACACGGTGTAGATACCAACTCTCTCGCTCTAAGCTTACCTCTGCTTGTGATTGAA 300
DB 81 ArgHisGlyAlaArgTyrProThrAspSerLeuGlyLysTyrSerAlaLeuIleGlu 100
QY 301 GCTATTCAAAGAACGCTACTGCTTTCAGGGTAAGTACGCTTCTTGAAGACTTACAAC 360
DB 101 GluIleGlnGlnAsnAlaThrThrPheAspGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 361 TACACTTGGTGTGACGACTGCTCACTCCATTCGTTGAAACCAAAATGTTAACTCTGT 420
DB 121 TyrSerLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 421 ATTAAGTCTACAGACATCAAGCTTTCGCTAGAAAGATCTTCCATTCATTCATGAGCT 480
DB 141 IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160
QY 481 TCTGGTCTTACAGAGTATTGCTTCTGCTGAAAGTTCATTCGAAGGTTTCCAAATCTGT 540
DB 161 SerGlySerArgValIleAlaSerGlyLysLysPheIleGluGlyPheGlnSerThr 160
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RESULT 15

US-09-233-310-32
Sequence 32, Application US/09233510
Patent No. 6350602

GENERAL INFORMATION:

APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veenstra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Seltin
TITLE OF INVENTION: Cloning and Expression of Microbial

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QY 541 AAGTTGGCTGACCCAGGTTCTCAACACACACCAAGCTTCTCCAGTTATTAACGTGATCAT 600
DB 191 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValIle 200
QY 601 CCAGAAGATCCGGTTACAACAACACACTTTGGACACGCTACTTGTACTCTTTCGAAGAC 660
DB 201 SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY 661 TCTGAATTAGGTGACGACGCTGAAGCTTAACCTCACTGCTTGTTCGCTCCAGCIATTAGA 720
DB 221 SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
QY 721 GCTAGATTGAAGCTGACTTGCAGGTTGTTACTTGTACTGACGACGACGCTGTTACTTG 780
DB 241 GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrTyrLeu 260
QY 781 ATGCACATGTGTCATTCGACACTGTGCTAGAACCTTCTGACGCTACTGAATTGTCTCA 840
DB 261 MetAspMetCysSerPheAspThrIleSerThrValAspThrLysLeuSerPro 280
QY 841 TTCTGCTTTGTTTCACTCAGCAGCAATGATGATCCATGCTTCAAGCTACTTGCAGGCTGG 900
DB 281 PheCysAspLeuPheThrHisAspGluTyrIleAsnTyrAspTyrLeuGlnSerLeuLys 300
QY 901 AAGTACTACGGTTACGGTGTGTAACCCATGGGTCACGCTCAAGCTCTGCTTCTGCTT 960
DB 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
QY 961 AACGAATTGATTGCTAGATTGACTCTCTCCAGTTCAAGACACACACCTCTACTAACCA 1020
DB 321 AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspThrSerSerAsnHis 340
QY 1021 ACTTGGACTCTAACCCAGCTACTTCCCATTTCAAGCTACTTGTACGCTGACTTCTCT 1080
DB 341 ThrLeuAspSerSerProAlaThrPheProLeuAspSerThrLeuTyrAlaAspPheSer 360
QY 1081 CACGACACACTATGATATCTATTTCTCGCTTGGTGTTCACACGCTACCAAGCCA 1140
DB 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380
QY 1141 TTGCTTACTTCTGTTGTAATCTATTGAAGAACTGACGGTACTTCTGCTTCTTGGACT 1200
DB 381 LeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaTyrThr 400
QY 1201 GTTCATTCGCTGCTAGAGTACGTACGTGAATGATGATCAATGTCAGCTGAAAGGAACCA 1260
DB 401 ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnPro 420
QY 1261 TTGTTAGATTTGGTTAACGACAGAGTTGTTCCATTCACCGCTTGTGCTGTTGACAAG 1320
DB 421 LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440
QY 1321 TTGGTGTAGATTGAAGACGACGACTTCGTTGAAGTTGTTGCTTTCGCTAGATCTGTGG 1380
DB 441 LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
QY 1381 AACTGGGCTGAATGTTTCGCT 1401
DB 461 AspTrpAlaGluCysPheAla 467
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Search completed: October 3, 2003, 08:57:09
Job time : 45.0567 secs

QY 351 EST-ETDGYAASWTVPFAARAYVENMOCQAGGGGEGEKEPLVRVLVNDVRVPLHGGGVD 409
DB 361 ESIEETDGYASASWTVPFGARAYVENMOCQA-----EKEPLVRVLVNDVRVPLHGGCAVD 413
QY 410 KLGRCKLDDFVEGLSFARSGGNWAECEFA 437
DB 414 KLGRCKRDDFVEGLSFARSGGNWAECEFA 441

RESULT 2

US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273.871A
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080.129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090.675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version: 4.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-634-493A-1

Query Match 87.0%; Score 2020; DB 4; Length 441;
Best Local Similarity 89.3%; Pred. No. 3.4e-207;
Matches 400; Conservative 10; Mismatches 20; Indels 18; Gaps 10;
QY 1 NSHSCDSTDVD-GYQC-PEISHLWGOYSPFFSLADESALSPOVPKRCRTVFQVLSRHGARY 58
DB 1 NSHSCDSTDVDGGYQCFPEISHLWGOYSPFFSLADESALSPOVPDCRVTFFQVLSRHGARY 60
QY 59 PTSSKSKYSALIERIOKNAT-FKGKYAFUKTYNTILGADDLTPFGENQMVNSGKIFYRR 117
DB 61 PTSSKSKYSALIERIOKNATFAFGKYAFUKTYNTILGADDLTPFGENQMVNSGKIFYRR 120
QY 118 YKALARNIVPFRASGSDRVITASAEKFTGFSQAKLADPA---HQASPVINVIIPEGSGY 174
DB 121 YKALARKIVPFRASGSDRVITASAEKFTGFSQAKLADPGSQPHQASPVIDVIIPEGSGY 180
QY 175 NNTLDHGLCTAFEDSTLGDDEANFTAVFAPPFIRARLEA-LPGVNLTDDEVNLMDCPF 233
DB 241 ETVARTSDATLSPPCDLFTADEW-QYDYLOSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
QY 291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFPFGALGYNGTAPLSTTSV 350
DB 301 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFPFGALGYNGTAPLSTTSV 360
QY 351 EST-ETDGYAASWTVPFAARAYVENMOCQAGGGGEGEKEPLVRVLVNDVRVPLHGGGVD 409
DB 361 ESIEETDGYASASWTVPFGARAYVENMOCQA-----EKEPLVRVLVNDVRVPLHGGCAVD 413
QY 410 KLGRCKLDDFVEGLSFARSGGNWAECEFA 437
DB 414 KLGRCKRDDFVEGLSFARSGGNWAECEFA 441

RESULT 3

US-09-273-871A-9
; Sequence 9, Application US/09273871-A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273.871A
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080.129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090.675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version: 4.0
; SEQ ID NO 9
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Variation
US-09-273-871A-9

Query Match 87.0%; Score 2020; DB 4; Length 467;
Best Local Similarity 89.3%; Pred. No. 3.4e-207;
Matches 400; Conservative 10; Mismatches 20; Indels 18; Gaps 10;
QY 1 NSHSCDSTDVD-GYQC-PEISHLWGOYSPFFSLADESALSPOVPKRCRTVFQVLSRHGARY 58
DB 27 NSHSCDSTDVDGGYQCFPEISHLWGOYSPFFSLADESALSPOVPDCRVTFFQVLSRHGARY 86
QY 59 PTSSKSKYSALIERIOKNAT-FKGKYAFUKTYNTILGADDLTPFGENQMVNSGKIFYRR 117
DB 87 PTSSKSKYSALIERIOKNATFAFGKYAFUKTYNTILGADDLTPFGENQMVNSGKIFYRR 146
QY 118 YKALARNIVPFRASGSDRVITASAEKFTGFSQAKLADPA---HQASPVINVIIPEGSGY 174
DB 147 YKALARKIVPFRASGSDRVITASAEKFTGFSQAKLADPGSQPHQASPVIDVIIPEGSGY 206
QY 175 NNTLDHGLCTAFEDSTLGDDEANFTAVFAPPFIRARLEA-LPGVNLTDDEVNLMDCPF 233
DB 207 NNTLDHGLCTAFEDSELGDDVEANFTALFAPFIRARLEADLPVTLDEDDVYVLMDCPF 266
QY 234 DTVARTSDATLSPPCDLFTADEW-QYDYLOSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
DB 267 ETVARTSDATLSPPCALFTDHEWRQDYLOSLCKYGYGAGNPLGPAQGVGFANETIAR 326
QY 291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFPFGALGYNGTAPLSTTSV 350
DB 327 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFPFGALGYNGTAPLSTTSV 386
QY 351 EST-ETDGYAASWTVPFAARAYVENMOCQAGGGGEGEKEPLVRVLVNDVRVPLHGGGVD 409
DB 387 ESIEETDGYASASWTVPFGARAYVENMOCQA-----EKEPLVRVLVNDVRVPLHGGCAVD 439
QY 410 KLGRCKLDDFVEGLSFARSGGNWAECEFA 437
DB 440 KLGRCKRDDFVEGLSFARSGGNWAECEFA 467

RESULT 4

US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:

APPLICANT: Lehmann, Martin
TITLE OF INVENTION: Consensus Phytases
FILE REFERENCE: consensus phytases 13239
CURRENT APPLICATION NUMBER: US/09/121,425
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: EPO 97112688.3
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 467
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-121-425-2

Query Match 81.9%; Score 1902; DB 3; Length 467;
Best Local Similarity 81.8%; Pred. No. 1.4e-194;
Matches 382; Conservative 10; Mismatches 19; Indels 56; Gaps 11;
QY 1 NSHSCDTVD-GVQC-PEISHLWGQYSPFSLADESAISPDVPGKCRVTFVQVLSRHGARY 58
DB 27 NSHSCDTVDGGYQCPEISHLWGQYSPFSLADESAISPDVPGKCRVTFVQVLSRHGARY 86
QY 59 PTSSKSKYKYSALIERIOKNATFKGYAFKTYNTLGADDLTPFGENQMVNSGKIFYRRY 118
DB 87 PTSSKSKAYS-----TYNTLGADDLTPFGENQMVNSGKIFYRRY 127
QY 119 KALARNIVPFVRASGSDRVIASAEKFIGFOSAKLADPA---HOASPVIN----- 165
DB 128 KALARKIVPFVRASGSDRVIASAEKFIGFOSAKLADPGSQPHQASPVIDLIFAIQKNAT 187
QY 166 -----VIIPGSGYNNLTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRLEA-L 214
DB 188 AFKGYAFKVIIPGSGYNNLTLDHGLCTAFEDSELGDDVEANFTALFAPAIRLEADL 247
QY 215 PGVNLTDEDVNLMDMCPDFTVARTSDATQLSPCDLFTADEW-OYDYLOSL-KYYGYGA 272
DB 248 PGVTLTDEDVYVLMDCPFETVARTSDATQLSPCALFTHDEWROYDYLOSLGKYYGYGA 307
QY 273 GNPLGPAQGVGF-NELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVS 331
DB 308 GNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVS 367
QY 332 IFPGLGNGTKPLSTTSVEST-ETDGYAASWTVPFAARAYVENMOCFAGGGGEGEKEP 390
DB 368 IFPGLGNGTKAPLSTTSVESTETDGYASASWTVPFGARAYVENMOCQA-----EKEP 420
QY 391 LVRVLNDRVPLRGCGVDKLGRCCKDDFVEGLSFARSGGNWAECEFA 437
DB 421 LVRVLNDRVPLRGCAVDKLGRCCKDDFVEGLSFARSGGNWAECEFA 467

RESULT 5
US-09-634-493A-2
Sequence 2, Application US/09634493A
Patent No. 6579975
GENERAL INFORMATION:
APPLICANT: Lehmann, Martin
TITLE OF INVENTION: Consensus Phytases
FILE REFERENCE: consensus phytases 13239
CURRENT APPLICATION NUMBER: US/09/634,493A
CURRENT FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: US/09/121,425
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: EPO 97112688.3
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 467

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-634-493A-2

Query Match 81.9%; Score 1902; DB 4; Length 467;
Best Local Similarity 81.8%; Pred. No. 1.4e-194;
Matches 382; Conservative 10; Mismatches 19; Indels 56; Gaps 11;
QY 1 NSHSCDTVD-GVQC-PEISHLWGQYSPFSLADESAISPDVPGKCRVTFVQVLSRHGARY 58
DB 27 NSHSCDTVDGGYQCPEISHLWGQYSPFSLADESAISPDVPGKCRVTFVQVLSRHGARY 86
QY 59 PTSSKSKYKYSALIERIOKNATFKGYAFKTYNTLGADDLTPFGENQMVNSGKIFYRRY 118
DB 87 PTSSKSKAYS-----TYNTLGADDLTPFGENQMVNSGKIFYRRY 127
QY 119 KALARNIVPFVRASGSDRVIASAEKFIGFOSAKLADPA---HOASPVIN----- 165
DB 128 KALARKIVPFVRASGSDRVIASAEKFIGFOSAKLADPGSQPHQASPVIDLIFAIQKNAT 187
QY 166 -----VIIPGSGYNNLTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRLEA-L 214
DB 188 AFKGYAFKVIIPGSGYNNLTLDHGLCTAFEDSELGDDVEANFTALFAPAIRLEADL 247
QY 215 PGVNLTDEDVNLMDMCPDFTVARTSDATQLSPCDLFTADEW-OYDYLOSL-KYYGYGA 272
DB 248 PGVTLTDEDVYVLMDCPFETVARTSDATQLSPCALFTHDEWROYDYLOSLGKYYGYGA 307
QY 273 GNPLGPAQGVGF-NELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVS 331
DB 308 GNPLGPAQGVGFANELIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTMVS 367
QY 332 IFPGLGNGTKPLSTTSVEST-ETDGYAASWTVPFAARAYVENMOCFAGGGGEGEKEP 390
DB 368 IFPGLGNGTKAPLSTTSVESTETDGYASASWTVPFGARAYVENMOCQA-----EKEP 420
QY 391 LVRVLNDRVPLRGCGVDKLGRCCKDDFVEGLSFARSGGNWAECEFA 437
DB 421 LVRVLNDRVPLRGCAVDKLGRCCKDDFVEGLSFARSGGNWAECEFA 467

RESULT 6
US-09-044-718-3
Sequence 3, Application US/09044718
Patent No. 6391605
GENERAL INFORMATION:
APPLICANT: KOSTREWA, Dirk
APPLICANT: PASAMONTES, Luis
APPLICANT: TOMSCHY, Andrea
APPLICANT: van LOON, Adolphus
APPLICANT: VOGEL, Kurt
APPLICANT: WYSS, Markus
TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: Modified Phytases
CURRENT APPLICATION NUMBER: US/09/044,718
CURRENT FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
PRIOR FILING DATE: 1997-03-25
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 439
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-09-044-718-3

Query Match 75.9%; Score 1762.5; DB 4; Length 439;
Best Local Similarity 77.4%; Pred. No. 1.1e-179;
Matches 345; Conservative 36; Mismatches 48; Indels 17; Gaps 10;

QY 2 SHSCDVTG-DYOC-PEISHLMGQYSPFFSLADESAISPDPKPGCRVTFVOVLSRHGARYP 59
1 SKSCDVTG-DYOC-PEISHLMGQYSPFFSLADESAISPDPKPGCRVTFVOVLSRHGARYP 60
QY 60 TSSKSKKYSALLERIQKAT-ERKGYAFKLTNYTLGADDTPEGENOMVNSGKIFRYR 116
Db 61 TSSKSKKYSALLERIQKAT-ERKGYAFKLTNYTLGADDTPEGENOMVNSGKIFRYR 120
QY 119 KALARNIPVFPVRSASDRVIAAEKFIETGFOAKLADP--AHOASPINVIIPGSGYNN 176
Db 121 KALARNIPVFPVRSASDRVIAAEKFIETGFOAKLADP--AHOASPINVIIPGSGYNN 180
QY 177 TLHGGLCTAFEDSTLGDAAENFTAVFAPPFIRAKLEA-LPGVNLTDDEVDVSLMDMCPEDT 235
Db 181 TLHGGLCTAFEDSTLGDAAENFTAVFAPPFIRAKLEA-LPGVNLTDDEVDVSLMDMCPEDT 240
QY 236 VARTSDATQSPFCDLFTADEW-OYDYLQSL-KYGYGAGNPLGPAQGVGF-NELIARLT 292
Db 241 VARTSDATQSPFCDLFTADEW-OYDYLQSL-KYGYGAGNPLGPAQGVGF-NELIARLT 300
QY 293 HSPVODHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFFALGLYNGTKPLSTTSVES 352
Db 301 HSPVODHTSTNHTLDSNPATFPLNATLYADFSDHNTMVSIFFALGLYNGTKPLSTTSVES 360
QY 353 I-ETDGYAASVTVPFAARAYVENMOCAGGGGEGEKEPELVRVLNDRVVPVHGGCGVDKL 411
Db 361 AKELDGYASASVVPFGARAYFEIMOCKS-----EKEPLVRALINDRVVPLHGGCGVDKL 413
QY 412 GRCKLDDFVEGLSPARSGNNAECFA 437
Db 414 GRCKLDDFVEGLSPARSGNNAECFA 439

RESULT 7

US-09-044-718-12

: Sequence 12, Application US/09044718

: Patent No. 6391505

: GENERAL INFORMATION:

: APPLICANT: KOSTREMA, Dirk

: APPLICANT: PASAMONTES, Luis

: APPLICANT: TOMSCHY, Andrea

: APPLICANT: van LOON, Adolphus

: APPLICANT: VOGEL, Mark

: APPLICANT: WYSS, Markus

: TITLE OF INVENTION: MODIFIED PHYTASES

: FILE REFERENCE: Modified Phytases

: CURRENT APPLICATION NUMBER: US/09/044,718

: CURRENT FILING DATE: 1998-03-19

: PRIOR APPLICATION NUMBER: EP 97810175.6

: PRIOR FILING DATE: 1997-03-25

: NUMBER OF SEQ ID NOS: 82

: SOFTWARE: PatentIn Ver. 2.1

: SEQ ID NO 12

: LENGTH: 449

: TYPE: PRI

: ORGANISM: Aspergillus fumigatus

US-09-044-718-12

Query Match 75.9%: Score 1762.5; DR 4; Length 449;

Best local similarity 77.4%: Pred. No. 1.le-179;

Matches 345; Conservative 36; Mismatches 48; Indels 17; Gaps 10;

QY 2 SHSCDVTG-DYOC-PEISHLMGQYSPFFSLADESAISPDPKPGCRVTFVOVLSRHGARYP 59
Db 11 SKSCDVTG-DYOC-PEISHLMGQYSPFFSLADESAISPDPKPGCRVTFVOVLSRHGARYP 70
QY 60 TSSKSKKYSALLERIQKAT-ERKGYAFKLTNYTLGADDTPEGENOMVNSGKIFRYR 118
Db 71 TSSKSKKYSALLERIQKAT-ERKGYAFKLTNYTLGADDTPEGENOMVNSGKIFRYR 130
QY 119 KALARNIPVFPVRSASDRVIAAEKFIETGFOAKLADP--AHOASPINVIIPGSGYNN 176
Db 131 KALARNIPVFPVRSASDRVIAAEKFIETGFOAKLADP--AHOASPINVIIPGSGYNN 190

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; LOCATION: 205
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 228
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 337
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 374
; OTHER INFORMATION: /note="potential N-glycosylation site"
; US-08-868-435-33

Query Match 75.9%; Score 1762.5; DB 3; Length 465;
Best Local Similarity 77.4%; Pred. No. 1.2e-179;
Matches 345; Conservative 36; Mismatches 48; Indels 17; Gaps 10;

Qy 2 SHSCDVID-GYOC-PEISHLWQYSPFFSLADESAISDVDPKGCRTFVOVLSRHGARYP 59
Db 27 SKSCDVIDLGQYOCSPATSHLWQYSPFFSLEDELSVSKLPKDCRITLVQVLSRHGARYP 86
Qy 60 TSSKSKKYSALIERIOKNAT-FKGKYAFKTYNTLGCADDLTDPFGNQMVNSGKIFYRY 118
Db 87 TSSKSKKYLVTIQANATDFGKFAFLKTYNTLGCADDLTDPFGQQLVNSGKIFYQRY 146
Qy 119 KALARNIVPVRASGSDRVIASAEKIEGFQSAKLADP--AHQASPVINVIPEGSGYNN 176
Db 147 KALARSVVPFIRASGSDRVIASGKIEGFQQAOKLADPGATNRAAPASIVPESETENN 206
Qy 177 TLDHGLCTAFEDSTLGDAAENFTAVFAPPARLEA-LPGVNLTDEDVNLMDMCPDET 235
Db 207 TLDHGVCCTFEASQLGDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVNSLMDMCSFT 266
Qy 236 VARTSDATQLSPFCDLTADW-QYDYLQSL-KYGYGAGNPLGPAQGVGF-NELIARLT 292
Db 267 VARTSDASQLSPFCQLFTHNEWKYNYLSGLKYYGYGAGNPLGPAQGVGF-NELIARLT 326
Qy 293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTWVSITFFALGLYNGTKPLSTTSVES 352
Db 327 RSPVQDHTSTNLSVNPATFPLNATMYVDFSDHNSMVSITFFALGLYNGTEPLSRTSVES 386
Qy 353 I-ETDGAASWVFPFAARAVENMOCCEAGSGGGEKEPLVRVLVNDVRVPLHGCQVDKL 411
Db 387 AKELDGISASWVFPFGARAFETWOCKS-----EKEPLVRALINDRVVPLRHGCDVDKL 439
Qy 412 GRCKLDLDFEGLSFARSGGNWAECEFA 437
Db 440 GRCKLNDLVKGLSWARSGGNWGECEFS 465

RESULT 9
US-08-744-231-33
; Sequence 33, Application US/08744231
; Patent No. 6358722
; GENERAL INFORMATION:
; APPLICANT: Van Loon, Adolphus
; APPLICANT: Mitchell, David
; TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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Db 327 RSPVQDHTSTNSTLVSNPATFPPLNATMYVDFSHDMSWVSIFFALGLYNGTEPLSRSTSVES 386
Qy 353 I-ETDGYAASWTVPFAARAYVEMMOCEAGGGGEGEKEPLRVLVNDRVVPVPLHGCGVDKL 411
Db 387 AKELDGYASWVVPFGARAYFETMOCKS-----EKEPLVRALINDRVVPLHGCGVDKL 439
Qy 412 GRCKLDDFVEGLSFARSGGNWAECEFA 437
Db 440 GRCKLDDFVKGLSWARSGGNWAECEFS 465

RESULT 10
US-09-044-718-78
; Sequence 78, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREMA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044.718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-78

Query Match 75.9%; Score 1762.5; DB 4; Length 465;
Best Local Similarity 77.4%; Pred. No. 1.2e-179;
Matches 345; Conservative 36; Mismatches 48; Indels 17; Gaps 10;

Qy 2 SHSCDITVD-GYQC-PEISHLWGQYSPFFSLADESALSIPVFKGCRVTFVQVLSRHGARYP 59
Db 27 SKSCDITVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLKPKDCRITLVQVLSRHGARYP 86
Qy 60 TSSKSKKYSALIERIOKNAT-FKGKYAFIKTYNTILGADDLTPFGENQMVNSGKIFKRY 118
Db 87 TSSKSKKYYKLVTAIQANATDFKGFAPLKTNYTILGADDLTPFGEQQLVNSGKIFKRY 146
Qy 119 KALARNIVPVRASGSDRVIASAEKTEGFSQAKLADP--AHQASPVINVIPEGSYNN 176
Db 147 KALARSVVPFIRASGSDRVIASGEKFEIGFQQAALADPGATNRAAPASVITPESEITFNN 206
Qy 177 TLHGCLCTAFEDSLGDAEAFNTAVFAPPIRARLEA-LPGVNLTDDEVVNLMDMCPEDT 235
Db 207 TLDHGVCCTKEASQLGDEVAANETALFADIRARAELHLPVLTDEDVVSLMDMCSFT 266
Qy 236 VARTSDATQLSPFCDLTADAW-OYDYLOSL-KYGYGAGNPLGPAQGVCF-NELIARLT 292
Db 267 VARTSDASQLSPFCQLTFHNEKKYNTLQSLGKYGYGAGNPLGPAQGGIGFTNELIARLT 326
Qy 293 HSPVQDHTSTNHTLDSNPATEPLNATLYADFSDNTMVSIFFALGLYNGTKPLSTTSVES 352
Db 327 RSPVQDHTSTNSTLVSNPATFPPLNATMYVDFSHDMSWVSIFFALGLYNGTEPLSRSTSVES 386
Qy 353 I-ETDGYAASWTVPFAARAYVEMMOCEAGGGGEGEKEPLRVLVNDRVVPVPLHGCGVDKL 411
Db 387 AKELDGYASWVVPFGARAYFETMOCKS-----EKEPLVRALINDRVVPLHGCGVDKL 439
Qy 412 GRCKLDDFVEGLSFARSGGNWAECEFA 437
Db 440 GRCKLDDFVKGLSWARSGGNWAECEFS 465

RESULT 12
US-09-273-871A-8
; Sequence 8, Application US/09273871A
; Patent No. 6514495
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/09/273.871A
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806

RESULT 11
US-09-636-499-6
; Sequence 6, Application US/09636499
; Patent No. 6475762
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; FILE REFERENCE: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC886-2
; CURRENT APPLICATION NUMBER: US/09/636.499
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148.960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-636-499-6

Query Match 75.9%; Score 1762.5; DB 4; Length 465;
Best Local Similarity 77.4%; Pred. No. 1.2e-179;
Matches 345; Conservative 36; Mismatches 48; Indels 17; Gaps 10;

Qy 2 SHSCDITVD-GYQC-PEISHLWGQYSPFFSLADESALSIPVFKGCRVTFVQVLSRHGARYP 59
Db 27 SKSCDITVDLGYQCSPATSHLWGQYSPFFSLEDELSVSSKLKPKDCRITLVQVLSRHGARYP 86
Qy 60 TSSKSKKYSALIERIOKNAT-FKGKYAFIKTYNTILGADDLTPFGENQMVNSGKIFKRY 118
Db 87 TSSKSKKYYKLVTAIQANATDFKGFAPLKTNYTILGADDLTPFGEQQLVNSGKIFKRY 146
Qy 119 KALARNIVPVRASGSDRVIASAEKTEGFSQAKLADP--AHQASPVINVIPEGSYNN 176
Db 147 KALARSVVPFIRASGSDRVIASGEKFEIGFQQAALADPGATNRAAPASVITPESEITFNN 206
Qy 177 TLHGCLCTAFEDSLGDAEAFNTAVFAPPIRARLEA-LPGVNLTDDEVVNLMDMCPEDT 235
Db 207 TLDHGVCCTKEASQLGDEVAANETALFADIRARAELHLPVLTDEDVVSLMDMCSFT 266
Qy 236 VARTSDATQLSPFCDLTADAW-OYDYLOSL-KYGYGAGNPLGPAQGVCF-NELIARLT 292
Db 267 VARTSDASQLSPFCQLTFHNEKKYNTLQSLGKYGYGAGNPLGPAQGGIGFTNELIARLT 326
Qy 293 HSPVQDHTSTNHTLDSNPATEPLNATLYADFSDNTMVSIFFALGLYNGTKPLSTTSVES 352
Db 327 RSPVQDHTSTNSTLVSNPATFPPLNATMYVDFSHDMSWVSIFFALGLYNGTEPLSRSTSVES 386
Qy 353 I-ETDGYAASWTVPFAARAYVEMMOCEAGGGGEGEKEPLRVLVNDRVVPVPLHGCGVDKL 411
Db 387 AKELDGYASWVVPFGARAYFETMOCKS-----EKEPLVRALINDRVVPLHGCGVDKL 439
Qy 412 GRCKLDDFVEGLSFARSGGNWAECEFA 437
Db 440 GRCKLDDFVKGLSWARSGGNWAECEFS 465

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: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: PA 1998 01176
: PRIOR FILING DATE: 1998-05-18
: PRIOR APPLICATION NUMBER: PA 1999 00091
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/080,129
: PRIOR FILING DATE: 1998-03-31
: PRIOR APPLICATION NUMBER: 60/090,675
: PRIOR FILING DATE: 1998-06-25
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 465
: TYPE: PRF
: ORGANISM: Aspergillus fumigatus
US-09-273,871A-B

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Query Match	75.94;	Score 1762.5;	DB 4;	Length 465;
Best Local Similarity	77.4%;	pred. N1.2e-179;		
Matches 345;	Conservative 36;	Mismatches 148;	Indels 17;	Gaps 10;
QY	2	SHSCDTVD-GVQC-PEISHLWGQVSPFSLADESAISPDVPGRCRVTFQVQLSRHGCARYP	59	
DB	27	SKSCDTVDLGYQCSPATSHLWGQVSPFSELEDSVSSKLPRDCRILLVQLSRHGCARYP	86	
QY	60	TSSKSKKYSALIERIQKNAT-FKQKYAFLKTYNTLGADDLTFFGENQMVNSGIKFYRRY	118	
DB	87	TSSKSKKYYKLVTAIQANATDFKQKFAFLKTYNTLGADDLTFFGSOQLVNSGIMFYQRY	146	
QY	119	KALARNIVPFRASGSDRVIASAEKFTFEGFSQAKLADP--AHOASPVINWIIPEGSGYNN	176	
DB	147	KALARSVVPFFIRASGSDRVIASGEKFTFEGFQQAKLADPGATNRAAPASIVIIPESETENN	206	
QY	177	LDHGLCTAFEDSTLGDDAEANFTAVPAPDIRARJEA-LPGVNLIDEDVVDLMDMCPEDT	235	
DB	207	LDHGVCTKFFASQLGDEVAANFTALPAPDIRARAEXHJFGVTLTDDEYVSLMDMCSFDT	266	
QY	236	VARTSDATOLSPEDCIFTADEW-QYDYQLSL-KYCYGAGNPLGPAGGVC-NELLIANT	292	
DB	267	VARTSDASQLSPFFCOLFTHREKKYNTLQSLGKYYGAGAGNPLGPAGGTGFTNELLIARIT	326	
QY	293	HSPVODHTSTNHTLDSNPATFPLNATLYAQSFDHNTMWSIFFALGLYNGIKPLSTISVES	352	
DB	327	RSPVODHTSTNST-VSNPATFPLNATMYVDFSHDNSMVSIFFAIGLYNGTEPLSXTSVES	386	
QY	353	I-ETDGYAASHTVPAAEAYVEMMOCEAGGGGEGEKEPLRVRLVNDRVVPLHGCQVSKL	411	
DB	387	AKELDGYASWVPGARAYPEIMOCKS-----EKEPLVRALVNDRVVPLHGCQVSKL	439	
QY	412	GRCKLDDDFEGLSFARSGGNMAECFA	437	
DB	440	GRCKLNDFFVKGLSWARSGGNMCEFS	465	

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RESULT 13
US-09-044-718-80
: Sequence 80, Application US/09044718
: Patent No. 6391505
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: CURRENT FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ IDS NOS: 82
: SOFTWARE: Patent in ver. 2.1

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: SEQ ID NO 80
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
: OS-09-044-718-80

Query Match: 75.6% Score 1754
Host Local Similarity 77.1% Pred. No.
Matches 344: Conservative 36; Mismatch

QY 2 SHSCDTVD-GYCC-PEISHLWGQYSPFFSL
DB 111111 1111 1111111111111111
QY 27 SKSCDTVDLGYCCSPATSHLWGQYSPFFSL
DB 111111 1111 1111111111111111
QY 60 TSSKSKYSALIERIQKWT-FKGYAFPLK
DB 111111 1111 1111111111111111
QY 87 TSSKSKYKKLVTAIQANATDFKGFAPLK
DB 111111 1111 1111111111111111
QY 119 KALARNIVPPFRASGSDRVIASAEKPIEGF
DB 111111 1111 1111111111111111
QY 147 KALARSVVPPFRASGSDRVIASGENFIEGF
DB 111111 1111 1111111111111111
QY 177 TLDHGLCTAFEDSTLGGDAENFTAVFAPP
DB 111111 1111 1111111111111111
QY 207 TLDHGVCTKFKFASQLGDEVAANFTALFAPD
DB 111111 1111 1111111111111111
QY 236 VARTSDATOLSPFVCDLFTADW-QYDIYLOS
DB 111111 1111 1111111111111111
QY 267 VARTSDASOLSPFCOLFTHNWKKNYLOS
DB 111111 1111 1111111111111111
QY 293 HSPVQDHTSTNHTLDSNPATPLNATLVAD
DB 111111 1111 1111111111111111
QY 327 RSPVQDHTSTNLTLSNPATPLNATMYVD
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QY 353 I-ETDGYAASVTVFAARAYVEMQCEAGG
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QY 387 AKELDGYASAMVPPGARAYPETMCKS--
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QY 412 GRCKLDQFVGLSFARSGNNNAECTA 437
DB 111111 1111 1111111111111111
QY 440 GRCKLDNFVGLSWARSGNNNGECFS 465
DB 111111 1111 1111111111111111

RESULT 14
US-09-044-718-79
: Sequence 79, Application US/03044718
: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: CURRENT FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97610175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 79
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
: OS-09-044-718-79

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Query Match 75.58; Score 1753.5; DB 4; Length 465;
Best Local Similarity 77.18; Pred. No. 1.1e-178;
Matches 344; Conservative 36; Mismatches 49; Indels 17; Gaps 10;
Qy 2 SHSCDTVD-GYQC-PEIETHLMQGVSPFSLADSESLSPDVPKGRVTFVQVLSRHGARYP 59

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Db 27 SKSCDVTDLGYQSPATSHLWGOYSPFFSLEDELSVSSKLKPKDCRIILVQVLSRHGARYP 86
Qy 60 TSSKSKYKYSALIERIOKNAT-FKGKYAFKLTNYTLGADDLTPFGENOMVNSGKIFYRRY 118
Db 87 TSSKSKYKYLVTAIQANATDFKGFAPLKTNYTLGADDLTPFGEOQLVNSGKIFYORY 146
Qy 119 KALARNIVPFVRASGSDRVIASAEKFTIEGQFQAKLADPGATNRAAPASVVIPESETENN 176
Db 147 KALARSVVPFIRASGSDRVIASGKFTIEGQFQAKLADPGATNRAAPASVVIPESETENN 206
Qy 177 TLDHGLCTAFEDSTLGDDAENFTAVFAPPRIARLEA-LPGVNLTDDEVDVNLMDMCPDCT 235
Db 207 TLDHGVCTKFEASQOLGDEVAANFTALFAPDIRARAKKHLPGVLTLDDEVDVSLMDMCSFDI 266
Qy 236 VARTSDATQSPFCDLFTADEW-OYDYLQSL-KYYGYGAGNPLGPAQGVGF-NEIARIAT 292
Db 267 VARTSDASOLSPPCOLFTHNEWKKNYLSGLKYYGYGAGNPLGPAQGVGF-NEIARIAT 326
Qy 293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352
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Qy 412 GRCKLDFEVLGSFARSGGNWACFA 437
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RESULT 15

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US-09-044-718-81
; Sequence 81, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044.718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 81
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-81
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Query Match 75.4%; Score 1750.5; DB 4; Length 465;
Best Local Similarity 76.9%; Pred. No. 2.3e-178;
Matches 343; Conservative 37; Mismatches 49; Indels 17; Gaps 10;
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Qy 2 SHSCDVTVD-GYQC-PEISHLWGOYSPFFSLEDELSAISFDVPGKGRVTFVQVLSRHGARYP 59
Db 27 SKSCDVTDLGYQSPATSHLWGOYSPFFSLEDELSVSSKLKPKDCRIILVQVLSRHGARYP 86
Qy 60 TSSKSKYKYSALIERIOKNAT-FKGKYAFKLTNYTLGADDLTPFGENOMVNSGKIFYRRY 118
Db 87 TSSKSKYKYLVTAIQANATDFKGFAPLKTNYTLGADDLTPFGEOQLVNSGKIFYORY 146
Qy 119 KALARNIVPFVRASGSDRVIASAEKFTIEGQFQAKLADPGATNRAAPASVVIPESETENN 176
Db 147 KALARSVVPFIRASGSDRVIASGKFTIEGQFQAKLADPGATNRAAPASVVIPESETENN 206
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Qy 177 TLDHGLCTAFEDSTLGDDAENFTAVFAPPRIARLEA-LPGVNLTDDEVDVNLMDMCPDCT 235
Db 207 TLDHGVCTKFEASQOLGDEVAANFTALFAPDIRARAKKHLPGVLTLDDEVDVSLMDMCSFDI 266
Qy 236 VARTSDATQSPFCDLFTADEW-OYDYLQSL-KYYGYGAGNPLGPAQGVGF-NEIARIAT 292
Db 267 VARTSDASOLSPPCOLFTHNEWKKNYLSGLKYYGYGAGNPLGPAQGVGF-NEIARIAT 326
Qy 293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 352
Db 327 RSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFALGLYNGTKPLSTTSVES 386
Qy 353 I-ETDGYAASWTVPFAARAYVENMOCAGGGGEGEKEPLVRVLVNDRVVPLHGGGVDKL 411
Db 387 AKELDGYASASWVVPFGARAYFETMCKS-----EKEPLVRALINDRVVPLHGGGVDKL 439
Qy 412 GRCKLDFEVLGSFARSGGNWACFA 437
Db 440 GRCKLDFVKGLSWARSGGNWGECEFS 465
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Job time : 14.1257 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:51 : Search time 99.8595 Seconds
(without alignments)
692.370 Million cell updates/sec

Title: US-09-488-265B-27

Perfect score: 2321

Sequence: 1 NSHSCDVTVDGQCPEISHLW.....DFVEGLSFARSGGNWAECA 437

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Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications_AA:*

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- 3: /cgn2.6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2.6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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- 16: /cgn2.6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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- 18: /cgn2.6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	1762.5	75.9	449	15	US-10-062-848-12
4	1762.5	75.9	465	14	US-10-083-452-8
5	1762.5	75.9	465	15	US-10-062-848-78
6	1762.5	75.9	465	15	US-10-229-358-6
7	1762.5	75.9	474	15	US-10-213-990-24
8	1754.5	75.6	465	15	US-10-062-848-80
9	1753.5	75.5	465	15	US-10-062-848-79
10	1750.5	75.4	465	15	US-10-062-848-81
11	1707.5	73.6	469	15	US-10-062-848-82
12	1684	72.6	444	15	US-10-062-848-1
13	1684	72.6	467	15	US-10-079-709-32
14	1684	72.6	467	15	US-10-229-358-5
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18	1672	72.0	467	9	US-09-929-060-3
19	1672	72.0	467	14	US-10-083-452-11
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21	1660	71.5	462	15	US-10-229-358-12
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23	1596.5	68.8	466	14	US-10-083-452-13
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36	1185	51.1	495	14	US-10-083-452-2
37	841	36.2	284	15	US-10-229-358-19
38	837.5	36.1	443	14	US-10-083-452-5
39	825	35.5	283	15	US-10-229-358-9
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43	793	34.2	442	14	US-10-083-452-4
44	663	28.6	212	15	US-10-229-358-16
45	372.5	16.6	312	15	US-10-229-358-21

ALIGNMENTS

RESULT 1
US-10-083-452-9
Sequence 9, Application US/10083452
Publication: No. US20020127218A1
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Phytase Variants
FILE REFERENCE: 5618,500-US
CURRENT APPLICATION NUMBER: US/10/083.452
CURRENT FILING DATE: 2002-02-26
PRIOR APPLICATION NUMBER: US/09/273.871
PRIOR FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: PA 1998 00407
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: PA 1998 00806
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: PA 1998 01176
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: PA 1999 00091
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/080,129
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/090,675
PRIOR FILING DATE: 1998-06-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 467
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Variation
US-10-083-452-9

Query Match 87.0%; Score 2020; DB 14; Length 467;

Best Local Similarity 89.3%; Pred. No. 6.3e-197;

Matches 400; Conservative 10; Mismatches 20; Indels 18; Gaps 10;


```
RESULT 6
US-10-229-358-6
; Sequence 6, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Trinci, Christian F.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US/10/229,358
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-229-358-6

Query Match      75.9%   Score 1762.5; DB 15; Length 465;
Best Local Similarity 77.4%; Pred. No. 1.1e-170;
Matches 345; Conservative 36; Mismatches 48; Indels 17; Gaps 10;

QY 2 SHSCOTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKCRVTFVQVLSRHGARYP 59
DB 27 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLELSVSSKLPKDCRITLVQVLSRHGARYP 86
QY 60 TSSKSKYKSLIETRIKQKAT-FKGKYAFKTYNTLGGADLTTPFGNOMVNSGKIFRYRY 118
DB 87 TSSKSKYKSLVTAIQANATDFKGFAPLKYNTLGGADLTTPFGQQLVNSGKIFRYRY 146
QY 119 KALARNIVPVFRASGSDRVIAASKEFTGFSQAKLADP--AHOASPVINVIIPEGSGYNN 176
DB 147 KALARSVVPFIRASGSDRVIAASKEFTGFSQAKLADP--AHOASPVINVIIPEGSETENN 206
QY 177 TLDHGLCTAREDTSLGDAEANTAVFAPPIDARLEA-LPGVNLTDVVDVNMDCPDET 235
DB 207 TLDHGVCTKFAESQGLGDEVAANTALFADPDIRAKKHLFGVTLTDEDVVSMDMCSFDT 266
QY 236 VARTSDATQSPFCDLTADDEW-QYDYLQSL-KYGYGAGNPLGPAQGVGF-NELIARLT 292
DB 267 VARTSDASQSPFCQLEFTHNWKYNYLSGLKYYGYGAGNPLGPAQGGIGFTNELIARLT 326
QY 293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFAFGLYNGTKPLSTTSVES 352
DB 327 RSPVQDHTSTNLTSLVSNPATFPLNATMYVDFSHDNTMVSIFFAFGLYNGTEPLSRTSVES 386
QY 353 I-ETDGYAASVTVPFAARAYVENMQCEAGGGGEGEKEPLRVLVNDRVVPLHGCGVDKL 411
DB 387 AKELDGYASVWVPFGARAYFETWCKS-----EKEPLVRLALINDRVVPLHGCGVDKL 439
QY 412 GRCKLDDEVEGLSFARSGGNWAECPA 437
DB 440 GRCKLNDVFKLSWARSNGNWGECFS 465

RESULT 7
US-10-213-990-24
; Sequence 24, Application US/10213990
; Publication No. US20030082595A1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Bo
; APPLICANT: Bussey, Howard
; APPLICANT: Storms, Reg
; APPLICANT: Roemer, Terry
; TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
; TITLE OF INVENTION: ENZYMES AND METHODS OF USE
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FILE REFERENCE: 10182-019-999
; CURRENT APPLICATION NUMBER: US/10/213,990
; CURRENT FILING DATE: 2002-08-05
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Aspergillus
US-10-213-990-24

Query Match      75.9%   Score 1762.5; DB 15; Length 474;
Best Local Similarity 77.4%; Pred. No. 1.1e-170;
Matches 345; Conservative 36; Mismatches 48; Indels 17; Gaps 10;

QY 2 SHSCDTVD-GYQC-PEISHLWGQYSPFFSLADESAISPDVPKCRVTFVQVLSRHGARYP 59
DB 36 SKSCDTVDLGYQCSPATSHLWGQYSPFFSLELSVSSKLPKDCRITLVQVLSRHGARYP 95
QY 60 TSSKSKYKSLIETRIKQKAT-FKGKYAFKTYNTLGGADLTTPFGNOMVNSGKIFRYRY 118
DB 96 TSSKSKYKSLVTAIQANATDFKGFAPLKYNTLGGADLTTPFGQQLVNSGKIFRYRY 155
QY 119 KALARNIVPVFRASGSDRVIAASKEFTGFSQAKLADP--AHOASPVINVIIPEGSGYNN 176
DB 156 KALARSVVPFIRASGSDRVIAASKEFTGFSQAKLADP--AHOASPVINVIIPEGSETENN 215
QY 177 TLDHGLCTAREDTSLGDAEANTAVFAPPIDARLEA-LPGVNLTDVVDVNMDCPDET 235
DB 216 TLDHGVCTKFAESQGLGDEVAANTALFADPDIRAKKHLFGVTLTDEDVVSMDMCSFDT 275
QY 236 VARTSDATQSPFCDLTADDEW-QYDYLQSL-KYGYGAGNPLGPAQGVGF-NELIARLT 292
DB 276 VARTSDASQSPFCQLEFTHNWKYNYLSGLKYYGYGAGNPLGPAQGGIGFTNELIARLT 335
QY 293 HSPVQDHTSTNHTLDSNPATFPLNATLYADFSHDNTMVSIFFAFGLYNGTKPLSTTSVES 352
DB 336 RSPVQDHTSTNLTSLVSNPATFPLNATMYVDFSHDNTMVSIFFAFGLYNGTEPLSRTSVES 395
QY 353 I-ETDGYAASVTVPFAARAYVENMQCEAGGGGEGEKEPLRVLVNDRVVPLHGCGVDKL 411
DB 396 AKELDGYASVWVPFGARAYFETWCKS-----EKEPLVRLALINDRVVPLHGCGVDKL 448
QY 412 GRCKLDDEVEGLSFARSGGNWAECPA 437
DB 449 GRCKLNDVFKLSWARSNGNWGECFS 474

RESULT 8
US-10-062-848-80
; Sequence 80, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREMA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
```

US-10-062-848-80

Query Match 75.6%; Score 1754.5; DB 15; Length 465;
Best Local Similarity 77.1%; Pred. No. 7.2e-170;
Matches 344; Conservative 36; Mismatches 49; Indels 17; Gaps 10;

```
QY 2 SHSCDVTVD-GYQC-PEISHLMGQYSPFFSLADESAISPDVPGKCRVTFVQVLSRHGARYP 59
DB 27 SKSCDVTDLGYQCSPATSHLMGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86
QY 60 TSSKSKKYKYSALIERIQKNAT-FKGYAFKLTNYTLGADDLTPFGENQMVNSGKIFYRRY 118
DB 87 TSSKSKKYKLVTAIOANADFKGKFAFLKTYNTLGGADDLTPFGEQQLVNSGKIFYORY 146
QY 119 KALARNIVPVRASGSDRVIASAEKFIQGFOSAKLADP--AHOASPVINVIIPGSGYNN 176
DB 147 KALARSVVPFIRASGSDRVIASGEKFIQGFQAKLADPGATNRAAPAIISVPIPESETFNN 206
QY 177 TLDHGLCTAFEDSTLGDAAENFTAVFAPPIRARLEA-LPGVNLTDDEVVNLMDKCPDT 235
DB 207 TLDHGVCCTFEASQGLDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVSLMDKCSFDI 266
QY 236 VARTSDATOLSPFCDLFTADEW-QYDYLSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
DB 267 VARTSDASQLSPFCQLFTHNWKYNYLSGLKYYGYGAGNPLGPAQGVGF-NELIARLT 326
QY 293 HSPVQDHTSTNLTLDNSNPATFPLNATLYADFSHNTWYSIFFALGLYNGTPLSTTSVES 352
DB 327 RSPVQDHTSTNLTSLVSNPATFPLNATMYVDFSHDMSVYSIFFALGLYNGTPLSTTSVES 386
QY 353 I-ETDGYAASWTVPFAARAYEMMOCEAGGGGGEKEPLVRVLVNDRVVPLHGGGVDKL 411
DB 387 AKELDYSASVWVPFCARAYFETMCKS-----EKESLVRLINDRVVPLHGGCDVZKL 439
QY 412 GRCKLDDFVEGLSFARSGGNWAECPA 437
DB 440 GRCKLNDFVKLSWARSGGNMGCEFS 465
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RESULT 9
US-10-062-848-79
: Sequence 79, Application US/10062848
: Publication No. US2003092155A1
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 79
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-10-062-848-79

Query Match 75.5%; Score 1753.5; DB 15; Length 465;
Best Local Similarity 77.1%; Pred. No. 9.1e-170;
Matches 344; Conservative 36; Mismatches 49; Indels 17; Gaps 10;

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QY 2 SHSCDVTVD-GYQC-PEISHLMGQYSPFFSLADESAISPDVPGKCRVTFVQVLSRHGARYP 59
DB 27 SKSCDVTDLGYQCSPATSHLMGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86
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QY 60 TSSKSKKYKYSALIERIQKNAT-FKGYAFKLTNYTLGADDLTPFGENQMVNSGKIFYRRY 118
DB 87 TSSKSKKYKLVTAIOANADFKGKFAFLKTYNTLGGADDLTPFGEQQLVNSGKIFYORY 146
QY 119 KALARNIVPVRASGSDRVIASAEKFIQGFOSAKLADP--AHOASPVINVIIPGSGYNN 176
DB 147 KALARSVVPFIRASGSDRVIASGEKFIQGFQAKLADPGATNRAAPAIISVPIPESETFNN 206
QY 177 TLDHGLCTAFEDSTLGDAAENFTAVFAPPIRARLEA-LPGVNLTDDEVVNLMDKCPDT 235
DB 207 TLDHGVCCTFEASQGLDEVAANFTALFAPDIRARAEKHLPGVTLTDEDVSLMDKCSFDI 266
QY 236 VARTSDATOLSPFCDLFTADEW-QYDYLSL-KYYGYGAGNPLGPAQGVGF-NELIARLT 292
DB 267 VARTSDASQLSPFCQLFTHNWKYNYLSGLKYYGYGAGNPLGPAQGVGF-NELIARLT 326
QY 293 HSPVQDHTSTNLTLDNSNPATFPLNATLYADFSHNTWYSIFFALGLYNGTPLSTTSVES 352
DB 327 RSPVQDHTSTNLTSLVSNPATFPLNATMYVDFSHDMSVYSIFFALGLYNGTPLSTTSVES 386
QY 353 I-ETDGYAASWTVPFAARAYEMMOCEAGGGGGEKEPLVRVLVNDRVVPLHGGGVDKL 411
DB 387 AKELDYSASVWVPFCARAYFETMCKS-----EKESLVRLINDRVVPLHGGCDVZKL 439
QY 412 GRCKLDDFVEGLSFARSGGNWAECPA 437
DB 440 GRCKLNDFVKLSWARSGGNMGCEFS 465
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RESULT 10
US-10-062-848-81
: Sequence 81, Application US/10062848
: Publication No. US2003092155A1
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 81
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Query Match 75.4%; Score 1750.5; DB 15; Length 465;
Best Local Similarity 76.9%; Pred. No. 1.8e-169;
Matches 343; Conservative 37; Mismatches 49; Indels 17; Gaps 10;

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QY 2 SHSCDVTVD-GYQC-PEISHLMGQYSPFFSLADESAISPDVPGKCRVTFVQVLSRHGARYP 59
DB 27 SKSCDVTDLGYQCSPATSHLMGQYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 86
QY 60 TSSKSKKYKYSALIERIQKNAT-FKGYAFKLTNYTLGADDLTPFGENQMVNSGKIFYRRY 118
DB 87 TSSKSKKYKLVTAIOANADFKGKFAFLKTYNTLGGADDLTPFGEQQLVNSGKIFYORY 146
QY 119 KALARNIVPVRASGSDRVIASAEKFIQGFOSAKLADP--AHOASPVINVIIPGSGYNN 176
DB 147 KALARSVVPFIRASGSDRVIASGEKFIQGFQAKLADPGATNRAAPAIISVPIPESETFNN 206
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Db 417 ALGRCIRDSFVRGLSFARSGGDWAECEFA 444

RESULT 13

US-10-079-709-32
; Sequence 32, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorkom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Sellen
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mortison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510
; FILING DATE: 20-JAN-1999
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-079-709-32

Query Match 72.6%; Score 1684; Db 15; Length 467;
Best Local Similarity 73.9%; Pred. No. 1.le-152;
Matches 331; Conservative 40; Mismatches 59; Indels 18; Gaps 10;
QY 1 NNSHCDTVD-GYQC-PEISHLWGQYSPFSLADESAISPDVPGKRVTFVGLSRHGARY 58
DB 27 NQSCDVTVDGQYCFSEISHLWGQYAPFFSLANESVISPEVPACRVTFVGLSRHGARY 86
QY 59 PTSSKSKKYSALIERIQKNA-TFKGYAFLKTYNYTLGADDLTPFGENQMVNSGKIFYRR 117
DB 87 PTDSKGGKYSALIEIQONATTFDGKYAFLKTYNYSLGADDLTPFGELVNSGKIFYR 146
QY 118 YKALARNIVFVRASGSDRVIASAEKFIQFQSAKIADP---AHQASPVINVIPEGSY 174
DB 147 YESLTRNIVPFRSSGSRVIAAGKFFIEGQSKLKDPRAPQGSQSPKIDVISEASS 206
QY 175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRABLE-ALPGVNLTDDEVNLMDCPF 233
DB 207 NNTLDPGCTVFEDESLADTVEANFTATFVPSIRQRENLSGVTLTDEVTYLMDCSF 266
QY 234 DTVARTSDATOLSPFCDLFTADEW-OYDYLOSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
DB 267 DTISTSTVDTKLSPFCDLFTHDEWINVDYLOSLKYYGCHGAGNPLGPTQGVYANELIAR 326
QY 291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTWYSIFFALGLYNGTKPLSTTSV 350
DB 327 LTHSPVHDDTSSNHTLDSNPATFPLNATLYADFSDHNTWYSIFFALGLYNGTKPLSTTSV 386
QY 351 ESI-ETDGYAASWTVPFAARAYVEMMOCEAGGGGEGEKEPLVRVLYNDRVPLHGCGVD 409
DB 387 ENITQDGFSSAWTVPFAARLYVEMMOCEA-----EQEPLVRVLYNDRVPLHGCGVD 439

QY 234 DIVARTSDATOLSPFCDLFTADEW-OYDYLOSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
DB 267 DTISTSTVDTKLSPFCDLFTHDEWINVDYLOSLKYYGCHGAGNPLGPTQGVYANELIAR 326
QY 291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTWYSIFFALGLYNGTKPLSTTSV 350
DB 327 LTHSPVHDDTSSNHTLDSNPATFPLNATLYADFSDHNTWYSIFFALGLYNGTKPLSTTSV 386
QY 351 ESI-ETDGYAASWTVPFAARAYVEMMOCEAGGGGEGEKEPLVRVLYNDRVPLHGCGVD 409
DB 387 ENITQDGFSSAWTVPFAARLYVEMMOCEA-----EQEPLVRVLYNDRVPLHGCGVD 439
QY 410 KIGRCKLDDFVEGLSFARSGGDWAECEFA 437
DB 440 ALGRCIRDSFVRGLSFARSGGDWAECEFA 467
RESULT 14
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ IDS NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-229-358-5

Query Match 72.6%; Score 1684; Db 15; Length 467;
Best Local Similarity 73.9%; Pred. No. 1.le-152;
Matches 331; Conservative 40; Mismatches 59; Indels 18; Gaps 10;
QY 1 NNSHCDTVD-GYQC-PEISHLWGQYSPFSLADESAISPDVPGKRVTFVGLSRHGARY 58
DB 27 NQSCDVTVDGQYCFSEISHLWGQYAPFFSLANESVISPEVPACRVTFVGLSRHGARY 86
QY 59 PTSSKSKKYSALIERIQKNA-TFKGYAFLKTYNYTLGADDLTPFGENQMVNSGKIFYRR 117
DB 87 PTDSKGGKYSALIEIQONATTFDGKYAFLKTYNYSLGADDLTPFGELVNSGKIFYR 146
QY 118 YKALARNIVFVRASGSDRVIASAEKFIQFQSAKIADP---AHQASPVINVIPEGSY 174
DB 147 YESLTRNIVPFRSSGSRVIAAGKFFIEGQSKLKDPRAPQGSQSPKIDVISEASS 206
QY 175 NNTLDHGLCTAFEDSTLGDDAEANFTAVFAPPIRABLE-ALPGVNLTDDEVNLMDCPF 233
DB 207 NNTLDPGCTVFEDESLADTVEANFTATFVPSIRQRENLSGVTLTDEVTYLMDCSF 266
QY 234 DTVARTSDATOLSPFCDLFTADEW-OYDYLOSL-KYYGYGAGNPLGPAQGVGF-NELIAR 290
DB 267 DTISTSTVDTKLSPFCDLFTHDEWINVDYLOSLKYYGCHGAGNPLGPTQGVYANELIAR 326
QY 291 LTHSPVQDHTSTNHTLDSNPATFPLNATLYADFSDHNTWYSIFFALGLYNGTKPLSTTSV 350
DB 327 LTHSPVHDDTSSNHTLDSNPATFPLNATLYADFSDHNTWYSIFFALGLYNGTKPLSTTSV 386
QY 351 ESI-ETDGYAASWTVPFAARAYVEMMOCEAGGGGEGEKEPLVRVLYNDRVPLHGCGVD 409
DB 387 ENITQDGFSSAWTVPFAARLYVEMMOCEA-----EQEPLVRVLYNDRVPLHGCGVD 439

GenScore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:51 : Search time 106.714 Seconds
(without alignments)
692.370 Million cell updates/sec

Title: US-09-488-265b-26
Perfect score: 2470
Sequence: 1 MGVFVLLSIATLFGSTSG7.....DFVEGLSFARSGGNWEEFA 467

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB5.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2311	93.6	467	14	US-10-083-452-9
2	1902	77.0	465	14	US-10-083-452-8
3	1902	77.0	465	15	US-10-062-848-78
4	1902	77.0	465	15	US-10-229-358-6
5	1895.5	76.7	474	15	US-10-213-990-24
6	1894	76.7	465	15	US-10-062-848-80
7	1893	76.6	465	15	US-10-062-848-79
8	1892.5	76.6	439	15	US-10-062-848-3
9	1892.5	76.6	449	15	US-10-062-848-12
10	1890	76.5	465	15	US-10-062-848-81
11	1868	75.6	469	15	US-10-062-848-82
12	1862	75.4	467	15	US-10-079-709-32
13	1862	75.4	467	15	US-10-229-358-5
14	1855	75.1	467	9	US-09-929-060-3
15	1850	74.9	467	14	US-10-083-452-11

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ALIGNMENTS

US-10-083-452-9
US-10-083-452-9
: Sequence 9, Application US/10083452
: Publication No. US2002012718A1
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: TITLE OF INVENTION: Phytase Variants
: FILE REFERENCE: 5618.500-US
: CURRENT APPLICATION NUMBER: US/10/083.452
: CURRENT FILING DATE: 2002-02-26
: PRIOR APPLICATION NUMBER: US/09/273.671
: PRIOR FILING DATE: 1999-03-22
: PRIOR APPLICATION NUMBER: PA 1998 00407
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: PA 1998 00806
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: PA 1998 01176
: PRIOR FILING DATE: 1998-09-18
: PRIOR APPLICATION NUMBER: PA 1999 00091
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/080,129
: PRIOR FILING DATE: 1998-03-31
: PRIOR APPLICATION NUMBER: 60/090,675
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 467
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Variation
US-10-083-452-9

Query Match 93.6% Score 2311; DB 14; Length 467;
Best Local Similarity 93.1%; Pred. No. 5.9e-225;
Matches 435; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy	1	MGVFWLLSIATLFGSTSGTALPRGNHSCDVTDDGYQCFPEISHLWGQVSPFFSLADE	60
Db	1	MGVFWLLSIATLFGSTSGTALPRGNHSCDVTDDGYQCFPEISHLWGQVSPFFSLEDE	60
Qy	61	SAISPDPKGRVTFVQVLSRPHGARVPTSSKSKKYSALTEAOKNATAFKGYAFLKTYN	120
Db	61	SAISPDPVDDCRVTFVQVLSRHGARVPTSSSKKAYSALTEAOKNATAFKGYAFLKTYN	120
Qy	121	YTLGADDLTPFGEQOMVNSGIKIFYRRYKALARKIVPFVIRASGSDRVIASAEKFIEGPOSA	180
Db	121	YTLGADDLTPFGEOMVNSGIKIFYRRYKALARKIVPFIRASGSDRVIASAEKFIEGPOSA	180
Qy	181	KLADPGANPHOASPIVNIYIPECAGYNNTLDHGCTAFTESELGGDDVFENFTAVTAPDIR	240
Db	181	KLADPGSOPHOASPIDVIYIPESGYNNTLDHGCTAFEDSELGGDDVEANFTAJEAPAIR	240
Qy	241	ARLEAHLPGVNLTDDEVVYVLMDCPFDTVARTSDATQLSPFCDLTFHDEWIDQYVLSLG	300
Db	241	ARLEADLPGVTLTDDEVVYVLMDCPFETVARTSDATESPFCALTFHDEWRQYVLSLG	300
Qy	301	KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVOOHTSTNHTLDSNPATPLNATLYAOFES	360
Db	301	KYYGYGAGNPLGPAQGVGFANELIARLTRSPVOOHTSTNHTLDSNPATPLNATLYAOFES	360
Qy	361	HONTMVISIFFALGLYNGTKPLUSTSVESIEETDGYAASMTVPFAARYVEMMOCAKEP	420
Db	361	HONSMTISIFFALGLYNGTAPLUSTSVESIEETDGYASMTVPFGARARYVEMMOCAKEP	420
Qy	421	LYRVLVNDRVVPLHGGGDKLGRCKRDDFVEGLSFARSGGNMEBCFA	467
Db	421	LYRVLVNDRVVPLHGGCAVDKLGRCRKDDFVEGLSFARSGGNMAEBCFA	467

```

RESULT 2
US-10-083-452-8
; Sequence 8, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618,500-US
; CURRENT APPLICATION NUMBER: US/10/083,452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00093
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-083-452-8

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Qy	61	SALSPDVPKCRVTVFOVL	SRHGARYPTSSKSKKYSALIEAIOKNATAPKGYAFLKTYN	120
Db	60	LSVSSKLPKDCRITLVQVL	SRHGARYPTSSKSKKYYKLIIVATQANATDKGKFAFLKTYN	119
Qy	121	YTLGADULITPFGEQOYVNSG	IKYRIRYKALARKIVPFRASGSDRVIASAKFTEGQSA	180
Db	120	YTLGADULITPFGEQOYVNSG	IKYRIRYKALARKIVPFRASGSDRVIASGEKFTGQQA	179
Qy	181	KLADPGANPHOASPV	WVLIIPGEGAGVNTLHGLCTAFEESELGDGVDEANTAVPAPPIR	240
Db	180	KLADPGAT-NRAAPASV	LIIPSESETFNNTLDGVCYKFEASOLGDVEAANTALFAPDIR	238
Qy	241	ARLEAHLPGVNLITDEDVYV	NLMDMCPEDTVARTSDATQLSPEGDIJTHDEWIOYDIQSLG	300
Db	239	ARAEKHLPGVLTDEDVYV	NLMDMCSFDTVARTSDASQLSPFCOLFTHEWKWKYVQSLG	298
Qy	301	KYGYGAGNPLGPAQGVGF	VNELLARIETHISPVODHTSTNHLDSNPATFPLNATLYADFES	360
Db	299	KYGYGAGNPLGPAQGI	GFTELARIETHISPVODHTSTNLSNPATFPLNAYWDFES	358
Qy	361	HONTWVSITFFALGLY	NGTKPLSTTSVESTTEEDGYAASMTVPFAARAVVEMQCEAKPEK	420
Db	359	HONSWVSITFFALGLY	NGTEPLESRITSVESAKELDGYASWVPFGARAVFETMCKSKPEK	418
Qy	421	LVRVLVNDRVVPLHGC	GVDRKGLGRCKRDXDFEGLSFARSOGGNWEECFA	467
Db	419	LYRVALINDRVVPLHGC	VDYKGLGRCKLNDYFVYGLSWARSOGGNWEECFS	466

```

RESULT 3
US-10-062-848-78
; Sequence 78, Application US/10062848
; Publication NO. US2030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphtus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatenLin Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-78

```

```

Query Match      77.0%  Score 1902;  DB 14;  Length 465;
Best Local Similarity 77.1%  Pred. No. 1.5e-183;
Matches 360;  Conservative 37;  Mismatches 68;  Indels 2;  Gaps 2;

Qy  1  MGVFVVLISLTIATLFGSTGALGRGSHSCSDVDGGYQCFPEISHLMGQYSPFSLADE 60
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db   1  MYTLFLLSAVLLSGRVSAAPSSAG--SKSCDVIDVGYCCSPATSHLMGQYSPFSLADE 59

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[illegible]


```
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn ver. 2.1
: SEQ ID NO 80
: LENGTH: 465
: TYPE: PR1
: ORGANISM: Aspergillus fumigatus
US-10-062-848-80

Query Match          76.7%  Score 1894;  DB 15;  Length 465;
Best Local Similarity 76.9%  Pred. No. 9.7e-183;
Matches 359;  Conservative 37;  Mismatches 69;  Indels 2;  Gaps 2;

QY 1 MGCVVLLSIATLFGSTSGTALGPRGNHSCDVTGCGYCFPEISHLWQXSPFSLADE 60
Db 1 MVTTLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYOCSPATSHLWQXSPFSLADE 59

QY 61 SAISPDVPKGRVTFVOVLGRHAGARYPTSSKKYKYSALIEATOKNATAFKGYAPLKTYN 120
Db 60 LSVSKLPGKDCRITLVOLVSRHAGARYPTSSKKYKYSALIEATOKNATDFKGFAPLKTYN 119

QY 121 YTLGADDLTPGEGQVMNSGKIFRYRYKALARKIVFVRASGSDRVIASAEKFIEGFOA 180
Db 120 YTLGADDLTPGEGQVMNSGKIFRYRYKALARKIVFVRASGSDRVIASAEKFIEGFOA 179

QY 181 KLADGANPHQASPVINVLIIPEGAGYNTLDHGLCTAFESSELGDDVEANTAFAPPIR 240
Db 180 KLADPGAT-NRAAPAIISVIIPESETFNILDHGCVTKFEASOLGDEVAANTAFAPDIR 238

QY 241 ARLEAHLPGVNLTDVYVNLMDMCPEDTVARTSDATQLSPPCDLFTHOFWTOYDYLOSLG 300
Db 239 ARAEKHLPGVLTLDVYVNLMDMCSFDTVARTSDASQSPFCOLFTHNEWKKNYLOSLG 298

QY 301 KYGYGAGNPLGPAQGVNFELTARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
Db 299 KYGYGAGNPLGPAQGVNFELTARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 358

QY 361 HDNTMVSTFFALGNGTKPLSTTSVESIEEDGYAASWTVPFAARAYVENMQCEAEKFP 420
Db 359 HDNSMVSTFFALGNGTKPLSTTSVESIEEDGYAASWTVPFAARAYVENMQCEAEKFP 418

QY 421 LVRVLNDRVYVPLHGCGVDKLGCRKRDFFVEGLSFARSGGNNEECFA 467
Db 419 LVRALINDRVYVPLHGCDVDKLGCRKLNDFVKGLSWARSGGNNGECFS 465

RESULT 7
US-10-062-848-79
: Sequence 79, Application US/10062848
: Publication No. US20030092155A1
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn ver. 2.1
: SEQ ID NO 3
: LENGTH: 439
: TYPE: PR1
: ORGANISM: Aspergillus fumigatus
```

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: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn ver. 2.1
: SEQ ID NO 79
: LENGTH: 465
: TYPE: PR1
: ORGANISM: Aspergillus fumigatus
US-10-062-848-79

Query Match          76.6%  Score 1893;  DB 15;  Length 465;
Best Local Similarity 76.9%  Pred. No. 1.2e-182;
Matches 359;  Conservative 37;  Mismatches 69;  Indels 2;  Gaps 2;

QY 1 MGCVVLLSIATLFGSTSGTALGPRGNHSCDVTGCGYCFPEISHLWQXSPFSLADE 60
Db 1 MVTTLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYOCSPATSHLWQXSPFSLADE 59

QY 61 SAISPDVPKGRVTFVOVLGRHAGARYPTSSKKYKYSALIEATOKNATAFKGYAPLKTYN 120
Db 60 LSVSKLPGKDCRITLVOLVSRHAGARYPTSSKKYKYSALIEATOKNATDFKGFAPLKTYN 119

QY 121 YTLGADDLTPGEGQVMNSGKIFRYRYKALARKIVFVRASGSDRVIASAEKFIEGFOA 180
Db 120 YTLGADDLTPGEGQVMNSGKIFRYRYKALARKIVFVRASGSDRVIASAEKFIEGFOA 179

QY 181 KLADGANPHQASPVINVLIIPEGAGYNTLDHGLCTAFESSELGDDVEANTAFAPPIR 240
Db 180 KLADPGAT-NRAAPAIISVIIPESETFNILDHGCVTKFEASOLGDEVAANTAFAPDIR 238

QY 241 ARLEAHLPGVNLTDVYVNLMDMCPEDTVARTSDATQLSPPCDLFTHOFWTOYDYLOSLG 300
Db 239 ARAEKHLPGVLTLDVYVNLMDMCSFDTVARTSDASQSPFCOLFTHNEWKKNYLOSLG 298

QY 301 KYGYGAGNPLGPAQGVNFELTARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 360
Db 299 KYGYGAGNPLGPAQGVNFELTARLTHSPVODHTSTNHTLDSNPATFPLNATLYADFS 358

QY 361 HDNTMVSTFFALGNGTKPLSTTSVESIEEDGYAASWTVPFAARAYVENMQCEAEKFP 420
Db 359 HDNSMVSTFFALGNGTKPLSTTSVESIEEDGYAASWTVPFAARAYVENMQCEAEKFP 418

QY 421 LVRVLNDRVYVPLHGCGVDKLGCRKRDFFVEGLSFARSGGNNEECFA 467
Db 419 LVRALINDRVYVPLHGCDVDKLGCRKLNDFVKGLSWARSGGNNGECFS 465

RESULT 8
US-10-062-848-3
: Sequence 3, Application US/10062848
: Publication No. US20030092155A1
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/10/062,848
: CURRENT FILING DATE: 2002-02-01
: PRIOR APPLICATION NUMBER: 09/044,718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn ver. 2.1
: SEQ ID NO 3
: LENGTH: 439
: TYPE: PR1
: ORGANISM: Aspergillus fumigatus
```

US-10-062-848-3

Query Match 76.6%; Score 1892.5; DB 15; Length 439;
Best Local Similarity 80.0%; Pred. No. 1.3e-182;
Matches 352; Conservative 37; Mismatches 50; Indels 1; Gaps 1;

QY 28 SHSCDVTGQYCFPEISHLMGQYSPFFSLADESAISPDVPGKCRVTFVQVLSRHGARYP 87
D 1 SKSCDVTDLGQYQCSPATSHLMGQYSPFFSLEDELSSKLPKDCR:TLVQVLSRHGARYP 60

QY 88 TSSSKKYKXKLVTAIONATDFKGFAPLKYNTYTLGADDLTPFGQQLVNSGIKFYRY 147
D 61 TSSSKKYKXKLVTAIONATDFKGFAPLKYNTYTLGADDLTPFGQQLVNSGIKFYRY 120

QY 148 KALARKIVPVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVNVIPEGAGYN 207
D 121 KALARSVVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVNVIPEGAGYN 207

QY 208 NLDHGLCTAFEESELCDDVEANFTAVFAPPIRARLEAHLPGVNLTDDEVNLMDCPFD 267
D 180 NLDHGLCTAFEESELCDDVEANFTAVFAPPIRARLEAHLPGVNLTDDEVNLMDCPFD 239

QY 268 TVARTSDATQSPCCDLTFHDEWIQDYQLSLGKYGYGAGNPLGPAQGVGFVNELIARL 327
D 240 TVARTSDATQSPCCDLTFHDEWIQDYQLSLGKYGYGAGNPLGPAQGVGFVNELIARL 299

QY 328 THSPVQDHTSTNHTLDSNPATFPLNATMYVDFSHDNTMVSIFPFGALGYNTEPLSRISVE 387
D 300 THSPVQDHTSTNHTLDSNPATFPLNATMYVDFSHDNTMVSIFPFGALGYNTEPLSRISVE 359

QY 388 SIETDGYAASWTVPFAARAYVENMQCEAEKEPLRVLVNDRVVPVPLHGCDVCKLGRCKLN 447
D 360 SAKELDGYASASWVVPFGARAYFETMQCKSEKEPLRVLRALINDRVVPLHGCDVCKLGRCKLN 419

QY 448 DFVEGLSFARSGGNWEECPA 467
D 420 DFVKGLSWARSGGNWEECPA 439

RESULT 9

US-10-062-848-12

; Sequence 12, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTRENA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-12

Query Match 76.6%; Score 1892.5; DB 15; Length 449;
Best Local Similarity 80.0%; Pred. No. 1.3e-182;
Matches 352; Conservative 37; Mismatches 50; Indels 1; Gaps 1;

QY 28 SHSCDVTGQYCFPEISHLMGQYSPFFSLADESAISPDVPGKCRVTFVQVLSRHGARYP 87
D 11 SKSCDVTDLGQYQCSPATSHLMGQYSPFFSLEDELSSKLPKDCR:ITLVQVLSRHGARYP 70

QY 88 TSSSKKYKXKLVTAIONATDFKGFAPLKYNTYTLGADDLTPFGQQLVNSGIKFYRY 147
D 71 TSSSKKYKXKLVTAIONATDFKGFAPLKYNTYTLGADDLTPFGQQLVNSGIKFYRY 130

QY 148 KALARKIVPVRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVNVIPEGAGYN 207
D 131 KALARSVVPFIRASGSDRVIASAEKFIEGFQSAKLADPGANPHQASPVNVIPEGAGYN 189

QY 208 NLDHGLCTAFEESELCDDVEANFTAVFAPPIRARLEAHLPGVNLTDDEVNLMDCPFD 267
D 190 NLDHGLCTAFEESELCDDVEANFTAVFAPPIRARLEAHLPGVNLTDDEVNLMDCPFD 249

QY 268 TVARTSDATQSPCCDLTFHDEWIQDYQLSLGKYGYGAGNPLGPAQGVGFVNELIARL 327
D 250 TVARTSDATQSPCCDLTFHDEWIQDYQLSLGKYGYGAGNPLGPAQGVGFVNELIARL 309

QY 328 THSPVQDHTSTNHTLDSNPATFPLNATMYVDFSHDNTMVSIFPFGALGYNTEPLSRISVE 387
D 310 THSPVQDHTSTNHTLDSNPATFPLNATMYVDFSHDNTMVSIFPFGALGYNTEPLSRISVE 369

QY 388 SIETDGYAASWTVPFAARAYVENMQCEAEKEPLRVLVNDRVVPVPLHGCDVCKLGRCKLN 447
D 370 SAKELDGYASASWVVPFGARAYFETMQCKSEKEPLRVLRALINDRVVPLHGCDVCKLGRCKLN 429

QY 448 DFVEGLSFARSGGNWEECPA 467
D 430 DFVKGLSWARSGGNWEECPA 449

RESULT 10

US-10-062-848-81

; Sequence 81, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTRENA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Query Match 76.5%; Score 1890; DB 15; Length 465;
Best Local Similarity 76.7%; Pred. No. 2.5e-182;
Matches 358; Conservative 38; Mismatches 69; Indels 2; Gaps 2;

QY 1 MCVFVLLSIATLFGSTSGTALGPNGNSHSCDVTGQYQCFPEISHLMGQYSPFFSLADE 6C
D 1 MVTLTFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGQYQCSPATSHLMGQYSPFFSLEDE 59

QY 61 SAISPDVPGKCRVTFVQVLSRHGARYPTSSSKKYKXKLVTAIONATDFKGFAPLKYNTY 120
D 60 VSSSKLPKDCR:ITLVQVLSRHGARYPTSSSKKYKXKLVTAIONATDFKGFAPLKYNTY 119

QY 121 YTLGADDLTPFGQQLVNSGIKFYRYKALARKIVPVRASGSDRVIASAEKFIEGFQSA 180
D 120 YTLGADDLTPFGQQLVNSGIKFYRYKALARSVVPFIRASGSDRVIASAEKFIEGFQSA 179

Db 61 SVISPEVPAGCVRVTAQVLSRHGARYPTDSKGGKYSALIEIQNATTFDCKYAFLLXYN 120
QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFVRASGRVVASAEKFTFEGFOSA 180
Db 121 YSLGADDLTPFGEQELVNSGKIFRYRYESLTNRNIVPFIRSSGSSRVATASGKKFTFEGFQST 180
QY 181 KLADPCANPHQASPVNVIIPGAGYNNI LNHGLCTAFEESEKADDOVEANFTAVFAPPIR 240
Db 181 KLKDPRAQPGQSPKIDVVISSASNNTLDPGTCTVFEDSELADTVEANFTAVFVPSIR 240
QY 241 ARLEAHLPGVNLTDVVDVNDMCPDFTVARTSDATQSPFCDLTFHDEWIQYDYLOSIG 300
Db 241 ORLENDLSGVLTDEVTYLMDCSFDITSTVDTKLSPPCDLTFHDEWINDYLOSIG 300
QY 301 KYGAGNPLGPAQGVFNELIARLTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFS 360
Db 301 KYGAGNPLGPTGCGVYANELIARLTHSPVHDUTSSNHTLDSNPATFPPLNSTLYADFS 360
QY 361 HONTMYSIFFALGLNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVENMOCEAKEP 420
Db 361 HONGIISILFALGLNGTKPLSTTIVENITQDGFSSAWTVPFASRLYVENMOCEAQEOP 420
QY 421 LVRVLNDRVPLHSCGVDKLGRCKRQDVEGLSFARSGGNWEECEFA 467
Db 421 LVRVLNDRVPLHGPCVDALGRCTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 13
US-10-229-358-5
; Sequence 5, Application US/10229358
; Publication No. US20030124700A1
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Irinici, Anthony P.J.
; TITLE OF INVENTION: Nucleic Acids Encoding
; TITLE OF INVENTION: Phytase Enzymes, and Host Cells Incorporating Same
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/10/229,358
; PRIOR FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-10-229-358-5

Query Match 75.4%; Score 1862; DB 15; Length 467;
Best Local Similarity 74.5%; Pred. No. 1.7e-179;
Matches 348; Conservative 44; Mismatches 75; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLFGSTSGIALGPRGNSHSCDVTGGYQCPPEISHLWQYSPFSLADE 60
Db 1 MGVSAYLLPLYLLSGVTSLGLAVPASRNOSTCUTVDGQYCFSETSHLWQYAPFSLANK 60
QY 61 SAISPDVPKGCVRVTVQVLSRHGARYPTSSSKKYSALIEATQKNATAFKGYAFLLKTYN 120
Db 61 SVISPEVPAGCVRVTAQVLSRHGARYPTDSKGGKYSALIEIQNATTFDCKYAFLLKTYN 120
QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFVRASGRVVASAEKFTFEGFOSA 180
Db 121 YSLGADDLTPFGEQELVNSGKIFRYRYESLTNRNIVPFIRSSGSSRVATASGKKFTFEGFQST 180
QY 181 KLADPCANPHQASPVNVIIPGAGYNNI LNHGLCTAFEESEKADDOVEANFTAVFAPPIR 240
Db 181 KLKDPRAQPGQSPKIDVVISSASNNTLDPGTCTVFEDSELADTVEANFTAVFVPSIR 240
QY 241 ARLEAHLPGVNLTDVVDVNDMCPDFTVARTSDATQSPFCDLTFHDEWIQYDYLOSIG 300
Db 241 ORLENDLSGVLTDEVTYLMDCSFDITSTVDTKLSPPCDLTFHDEWINDYLOSIG 300

QY 301 KYGAGNPLGPAQGVFNELIARLTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFS 360
Db 301 KYGAGNPLGPTGCGVYANELIARLTHSPVHDUTSSNHTLDSNPATFPPLNSTLYADFS 360
QY 361 HONTMYSIFFALGLNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVENMOCEAKEP 420
Db 361 HONGIISILFALGLNGTKPLSTTIVENITQDGFSSAWTVPFASRLYVENMOCEAQEOP 420
QY 421 LVRVLNDRVPLHSCGVDKLGRCKRQDVEGLSFARSGGNWEECEFA 467
Db 421 LVRVLNDRVPLHGPCVDALGRCTRDSFVRGLSFARSGGDWAECEFA 467

RESULT 14
US-09-929-060-3
; Sequence 3, Application US/0992906C
; Patent No. US20030068350A1
; GENERAL INFORMATION:
; APPLICANT: KONDO, HIEMASA
; APPLICANT: ANAZAWA, HIDEHARU
; APPLICANT: KANEKO, SYUNICHI
; APPLICANT: NAGASHIMA, TADASHI
; APPLICANT: TANGE, TATSUYA
; TITLE OF INVENTION: NOVEL PHYTASE AND GENE ENCODING SAID PHYTASE
; FILE REFERENCE: 081356/0166
; CURRENT APPLICATION NUMBER: US/09/929,060
; CURRENT FILING DATE: 2001-08-05
; PRIOR APPLICATION NUMBER: 09/543,744
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 09/155,855
; PRIOR FILING DATE: 1998-10-05
; PRIOR APPLICATION NUMBER: JP 084314/1996
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus niger
US-09-929-060-3

Query Match 75.1%; Score 1855; DB 9; Length 467;
Best Local Similarity 73.4%; Pred. No. 8.7e-179;
Matches 343; Conservative 51; Mismatches 73; Indels 0; Gaps 0;

QY 1 MGVFVLLSIATLFGSTSGIALGPRGNSHSCDVTGGYQCPPEISHLWQYSPFSLADE 60
Db 1 MGVSAYLLPLYLLSGVTSLGLAVPASRNOSTCUTVDGQYCFSETSHLWQYAPFSLANK 60
QY 61 SAISPDVPKGCVRVTVQVLSRHGARYPTSSSKKYSALIEATQKNATAFKGYAFLLKTYN 120
Db 61 SAISPDVPAGCVRVTAQVLSRHGARYPTDSKGGKYSALIEIQNATTFDCKYAFLLKTYN 120
QY 121 YTLGADDLTPFGEQOMVNSGKIFRYRYKALARKIVPFVRASGRVVASAEKFTFEGFOSA 180
Db 121 YSLGADDLTPFGEQELVNSGKIFRYRYESLTNRNIVPFIRSSGSSRVATASGKKFTFEGFQST 180
QY 181 KLADPCANPHQASPVNVIIPGAGYNNI LNHGLCTAFEESEKADDOVEANFTAVFAPPIR 240
Db 181 KLKDPRAQPGQSPKIDVVISSASNNTLDPGTCTVFEDSELADTVEANFTAVFVPSIR 240
QY 241 ARLEAHLPGVNLTDVVDVNDMCPDFTVARTSDATQSPFCDLTFHDEWIQYDYLOSIG 300
Db 241 ORLENDLSGVLTDEVTYLMDCSFDITSTVDTKLSPPCDLTFHDEWINDYLOSIG 300
QY 301 KYGAGNPLGPAQGVFNELIARLTHSPVQDHTSTNHTLDSNPATFPPLNATLYADFS 360
Db 301 KYGAGNPLGPTGCGVYANELIARLTHSPVHDUTSSNHTLDSNPATFPPLNSTLYADFS 360
QY 361 HONTMYSIFFALGLNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVENMOCEAKEP 420
Db 361 HONGIISILFALGLNGTKPLSTTIVENITQDGFSSAWTVPFASRLYVENMOCEAQEOP 420

Search completed: October 3, 2003, 08:12:28
Job time : 108.714 secs

RESULT 15
US-10-083-452-11

Query Match	74.9%	Score 1850;	DB 14;	Length 467;
Best Local Similarity	74.1%	Pred. No. 2.8e-177;		
Matches 346;	Conservative 44;	Mismatches 477;	Indels 0;	Gaps 0;
Qy	1	MGVYVVLLSIATLFGSTSGTALPGRNHSCDITVDGQYCFPEISHLMQGYSPFFSLADE	60	
Db	1	MGVSAILPLVLLSVTSSGLAVPASRNQSCDITVQYQCFSETSHLMQYAPFFSLANE	60	
Qy	61	SAISDPVPGKGRVTFVQVLSRHGARYPTSSKKKYSALIEALOKNATAFKGYAFELKYN	120	
Db	61	SWISPEVPAGCRVTFQAQVLSRHGARYPTDSKGGKYSALIEEIQONATTFDGKYAFELKYN	120	
Qy	121	YTLGADDLTPFGEQOMVNSGKFKFYRYKALARKTVPPVRASGSDRYVIAEAKFIEGQPSA	180	
Db	121	YSLGADDLTPFGEQELVNSGKFKFYRYESLTRNLVPPIRSGSSRVIAEAKFIEGFJST	180	
Qy	181	KIADPGANPHQASPVINVIIEPGAGYNNTLDHGLCTAFPESESLGDDVEANFTAVZAPPIR	240	
Db	181	KLKDPRAQPGQSSPKIDVVI SEASSNNTLDPGTCTVFDESELADVEANFTATFVPSIR	240	
Qy	241	ARLEAHLPGVNLTDEBVNLMDMCPFDITVARTSDATLSPECDFETHDEWIOVDYLOSLG	300	
Db	241	QRLENDLSGVTLTOTEVTVLMDMCSPTISTSTVDTKLSFPCDLFTHDEWINVDYLOSLK	300	
Qy	301	KYYGYGAGNPLGPAQGVGFVNELIARLTHSPVDHSTINHTLDSNPATPLNATLYAQFS	360	
Db	301	KYYGHGAGNPLGPTQGVGYANELIARLTHSPVHDTSNNHTLDSNPATPLKSTLYAQFS	360	
Qy	361	HDNTMYSIFFALGLNGTKPLSTTSVESIEETDGYAASWTVPFAARYVEMMOCEAKEP	420	
Db	361	HDNGIISIIIFALGLNGTKPLSTTTVENITOTDGFSSANTVPFAARKLYVEMMCCQAEAP	420	
Qy	421	LVRVLVNDRVPLHCGGVDKLGRCKRDDFVEGLGSFARSGGNWEECA	467	
Db	421	LVRVLVNDRVWPLHRCPPVDALGRCTROSFVRLGSLSFARSGGDWAECA	467	

GenCore version 5.1.16
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OM protein - protein search, using sw model

Run on: October 3, 2003, 07:46:45 ; Search time 12.9581 Seconds
(without alignments)
1524.850 Million cell updates/sec

Title: US-09-488-265B-26
Perfect score: 2470
Sequence: 1 MGVEVLLSLATLFGSTG.....DFEGLSFGSGNMEECA 467

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCUTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2311	93.6	467	US-09-273-871A-9	Sequence 9, Appl
2	2185	88.5	441	US-09-121-425-1	Sequence 1, Appl
3	2185	88.5	441	US-09-634-493A-1	Sequence 1, Appl
4	2173	88.0	467	US-09-121-425-2	Sequence 2, Appl
5	2173	88.0	467	US-09-634-493A-2	Sequence 2, Appl
6	1902	77.0	465	US-08-868-435-33	Sequence 33, Appl
7	1902	77.0	465	US-08-744-231-33	Sequence 33, Appl
8	1902	77.0	465	US-09-044-718-78	Sequence 78, Appl
9	1902	77.0	465	US-09-636-499-6	Sequence 6, Appl
10	1902	77.0	465	US-09-273-871A-8	Sequence 8, Appl
11	1894	76.7	465	US-09-044-718-80	Sequence 80, Appl
12	1893	76.6	465	US-09-044-718-79	Sequence 79, Appl
13	1892.5	76.6	439	US-09-044-718-3	Sequence 3, Appl
14	1892.5	76.6	439	US-09-044-718-12	Sequence 12, Appl
15	1890	76.5	465	US-09-044-718-81	Sequence 81, Appl
16	1868	75.6	469	US-09-044-718-82	Sequence 82, Appl
17	1866	75.5	467	US-07-923-724-8	Sequence 8, Appl
18	1866	75.5	467	US-08-609-426A-8	Sequence 8, Appl
19	1866	75.5	467	US-08-374-652C-2	Sequence 2, Appl
20	1862	75.4	467	US-08-151-574-32	Sequence 32, Appl
21	1862	75.4	467	US-08-146-424-20	Sequence 20, Appl
22	1862	75.4	467	US-08-693-709-2	Sequence 2, Appl
23	1862	75.4	467	US-08-419-448-32	Sequence 32, Appl
24	1862	75.4	467	US-08-819-825-3	Sequence 3, Appl
25	1862	75.4	467	US-09-163-842-3	Sequence 3, Appl
26	1862	75.4	467	US-09-233-510-32	Sequence 32, Appl
27	1862	75.4	467	US-09-636-499-5	Sequence 5, Appl

28	1855	75.1	467	3	US-09-155-855-3	Sequence 3, Appl
29	1855	75.1	467	4	US-09-543-744-3	Sequence 3, Appl
30	1855	75.1	467	4	US-09-929-060-3	Sequence 3, Appl
31	1850	74.9	467	4	US-09-273-871A-11	Sequence 11, Appl
32	1843	74.6	462	4	US-09-636-499-12	Sequence 12, Appl
33	1841	74.5	466	3	US-08-868-435-12	Sequence 12, Appl
34	1841	74.5	466	4	US-08-744-231-12	Sequence 12, Appl
35	1826	73.9	466	3	US-08-868-435-35	Sequence 35, Appl
36	1826	73.9	466	4	US-08-744-231-35	Sequence 35, Appl
37	1820	73.7	444	4	US-09-044-718-1	Sequence 1, Appl
38	1813.5	73.4	463	3	US-08-868-435-23	Sequence 23, Appl
39	1813.5	73.4	463	4	US-08-744-231-29	Sequence 29, Appl
40	1813.5	73.4	463	4	US-09-273-871A-10	Sequence 10, Appl
41	1813	73.4	443	3	US-09-155-855-1	Sequence 1, Appl
42	1813	73.4	443	4	US-09-543-744-1	Sequence 1, Appl
43	1813	73.4	443	4	US-09-929-060-1	Sequence 1, Appl
44	1808	73.2	443	3	US-09-155-855-2	Sequence 2, Appl
45	1808	73.2	443	4	US-09-543-744-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-273-871A-9

; Sequence 9, Application US/09273871A

; Patent No. 6514495

; GENERAL INFORMATION:

; APPLICANT: Svendsen, Allan

; TITLE OF INVENTION: Phytase Variants

; FILE REFERENCE: 5618.500-US

; CURRENT APPLICATION NUMBER: US/09/273,871A

; CURRENT FILING DATE: 1999-03-22

; PRIOR APPLICATION NUMBER: PA 1998 00407

; PRIOR FILING DATE: 1998-03-23

; PRIOR APPLICATION NUMBER: PA 1998 00806

; PRIOR FILING DATE: 1998-06-19

; PRIOR APPLICATION NUMBER: PA 1998 01176

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: PA 1999 00091

; PRIOR FILING DATE: 1999-01-22

; PRIOR APPLICATION NUMBER: 60/080,125

; PRIOR FILING DATE: 1998-03-31

; PRIOR APPLICATION NUMBER: 60/090,675

; PRIOR FILING DATE: 1998-06-25

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 467

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Variation

US-09-273-871A-9

Query Match 93.6%; Score 2311; DB 4; Length 467;

Best Local Similarity 93.1%; Pred. No. 3.9e+235;

Matches 435; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Cy 1 MGVEVLLSLATLFGSTGALSPRGNSHSCDVGQYOCFPE:SHLWGQYSPFFSLADE 60

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Db 1 MGVEVLLSLATLFGSTGALSPRGNSHSCDVGQYOCFPE:SHLWGQYSPFFSLEDE 60

|||||

Qy 61 SATSPDVPKCCRTTFQVLSRHGARYPTSSSKKYSALIEAIQKNATAFKGYAPFLKTYN 120

|||||

Db 61 SATSPDVPDCCRTTFQVLSRHGARYPTSSSKSKYASALIEAIQKNATAFKGYAPFLKTYN 120

|||||

Qy 121 YTLGADDLTPFGQQQMVNSGINKFYRYKALARKIVPFVRASGSDRVIASAEKFIQSFQSA 180

|||||

Db 121 YTLGADDLTPFGQNMVNSGINKFYRYKALARKIVPFIRASGSDRVIASAEKFIQSFQSA 180

|||||

Qy 181 KLADGANPHOASPVINVIPEGAGYNNLTDLGLCTAFEESELGDODVEANTAVFAPPIR 240

|||||

Db 181 KLADPGSQHQASPVIDVITPEGSGYNNNTLDHGTCTAFEDSELGDDVEANFTALFAPAIR 240
Qy 241 ARLEAHLPGVNLTDDEVDVNLMDMCPDFTVARTSDATOLSPCDLFTHDEWQYXYLSLG 300
Db 241 ARLEADPGVTLDEVDVYLMDCMCFETVARTSDATELSFPCALFTHDENRQYDYLSLG 300
Qy 301 KYGYGAGNPLGPAOGVGFVFNELIARLTHSPYODHTSTNHTJDSNPATFPLNATLYADFS 360
Db 301 KYGYGAGNPLGPAOGVGFVFNELIARLTHSPYODHTSTNHTJDSNPATFPLNATLYADFS 360
Qy 361 HDNMTWSIFALGLYNGIKPFLSTTSVESTERTDGYAASWTVPFAARAYVENMOCEAKEP 420
Db 361 HDNMTWSIFALGLYNGIKPFLSTTSVESTERTDGYAASWTVPFAARAYVENMOCEAKEP 420
Qy 421 LVRVLVNDVRVPLRGCGVOKLGRCKRDFVEGLSFARSGGNWEECEFA 467
Db 421 LVRVLVNDVRVPLRGCGVOKLGRCKRDFVEGLSFARSGGNWEECEFA 467

RESULT 2
US-09-121-425-1
; Sequence 1, Application US/0912:425
; Patent No. 6153418
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; FILE REFERENCE: Consensus Phytases
; CURRENT APPLICATION NUMBER: US/09/121,425
; PRIOR FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: EPO 97112688.3
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-121-425-1

Query Match 88.5%; Score 2185; DB 3; Length 441;
Best Local Similarity 92.7%; Pred. No. 7.1e-222;
Matches 409; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 27 NSHSCDVTDDGYQCQFPEISHLWGQYSPFFSLADESAISPDVPKGCRTVQVLSRHGARY 86
Db 1 NSHSCDVTDDGYQCQFPEISHLWGQYSPFFSLEDESAISPDVPDCCRVTTFVQVLSRHGARY 60
Qy 87 PTSSKSKYSALIEAIQKNATAFKGYAFKTYNTYLGADDLTPFGEOMVNSGKEYR 146
Db 61 PTSSKSKAYSALIEAIQKNATAFKGYAFKTYNTYLGADDLTPFGENQMVNSGKEYR 120
Qy 147 YKALARKIVPVRASGSDRVIASAEKFIQFQSAKLADPCANPHQASPVINVLPEGAGY 206
Db 121 YKALARKIVPVRASGSDRVIASAEKFIQFQSAKLADPCANPHQASPVINVLPEGAGY 180
Qy 207 NNTLDHGCTAFESSELGDDVEANFTAVFAPPIRARLEADLPGVTLTDEDVYVLMDCPF 240
Db 181 NNTLDHGCTAFESSELGDDVEANFTALFAPAIRLEADLPGVTLTDEDVYVLMDCPF 240
Qy 267 DTVARTSDATOLSPCDLFTHDEWQYDYLSLGKYYGYGAGNPLGPAOGVGFVFNELIAR 326
Db 241 ETVARISDATLSFPCALFTHDENRQYDYLSLGKYYGYGAGNPLGPAOGVGFVFNELIAR 300
Qy 327 LTHSPYODHTSTNHTJDSNPATFPLNATLYADFSHNTWYSIFFALGLYNGIKPLSTTSV 386
Db 301 LTRSPYODHTSTNHTJDSNPATFPLNATLYADFSHNSMISIFFALGLYNGIKPLSTTSV 360
Qy 387 ESIEETDGYAASWTVPFAARAYVENMOCEAKEPLVRVLVNDVRVPLRGCGVOKLGRCKR 446
Db 361 ESIEETDGYAASWTVPFAARAYVENMOCEAKEPLVRVLVNDVRVPLRGCGVOKLGRCKR 420

Qy 447 DDFVEGLSFARSGGNWEECEFA 467
Db 421 DDFVEGLSFARSGGNWEECEFA 441

RESULT 3
US-09-634-493A-1
; Sequence 1, Application US/09634493A
; Patent No. 6579975
; GENERAL INFORMATION:
; APPLICANT: Lehmann, Martin
; FILE REFERENCE: Consensus Phytases
; CURRENT APPLICATION NUMBER: US/09/634,493A
; PRIOR FILING DATE: 2000-08-08
; PRIOR APPLICATION NUMBER: US/09/121,425
; PRIOR FILING DATE: 1998-07-23
; PRIOR APPLICATION NUMBER: EPO 97112688.3
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:consensus
; OTHER INFORMATION: sequence
US-09-634-493A-1

Query Match 88.5%; Score 2185; DB 4; Length 441;
Best Local Similarity 92.7%; Pred. No. 7.1e-222;
Matches 409; Conservative 13; Mismatches 19; Indels 0; Gaps 0;

Qy 27 NSHSCDVTDDGYQCQFPEISHLWGQYSPFFSLADESAISPDVPKGCRTVQVLSRHGARY 86
Db 1 NSHSCDVTDDGYQCQFPEISHLWGQYSPFFSLEDESAISPDVPDCCRVTTFVQVLSRHGARY 60
Qy 87 PTSSKSKYSALIEAIQKNATAFKGYAFKTYNTYLGADDLTPFGEOMVNSGKEYR 146
Db 61 PTSSKSKAYSALIEAIQKNATAFKGYAFKTYNTYLGADDLTPFGENQMVNSGKEYR 120
Qy 147 YKALARKIVPVRASGSDRVIASAEKFIQFQSAKLADPCANPHQASPVINVLPEGAGY 206
Db 121 YKALARKIVPVRASGSDRVIASAEKFIQFQSAKLADPCANPHQASPVINVLPEGAGY 180
Qy 207 NNTLDHGCTAFESSELGDDVEANFTAVFAPPIRARLEADLPGVTLTDEDVYVLMDCPF 240
Db 181 NNTLDHGCTAFESSELGDDVEANFTALFAPAIRLEADLPGVTLTDEDVYVLMDCPF 240
Qy 267 DTVARTSDATOLSPCDLFTHDEWQYDYLSLGKYYGYGAGNPLGPAOGVGFVFNELIAR 326
Db 241 ETVARISDATLSFPCALFTHDENRQYDYLSLGKYYGYGAGNPLGPAOGVGFVFNELIAR 300
Qy 327 LTHSPYODHTSTNHTJDSNPATFPLNATLYADFSHNTWYSIFFALGLYNGIKPLSTTSV 386
Db 301 LTRSPYODHTSTNHTJDSNPATFPLNATLYADFSHNSMISIFFALGLYNGIKPLSTTSV 360
Qy 387 ESIEETDGYAASWTVPFAARAYVENMOCEAKEPLVRVLVNDVRVPLRGCGVOKLGRCKR 446
Db 361 ESIEETDGYAASWTVPFAARAYVENMOCEAKEPLVRVLVNDVRVPLRGCGVOKLGRCKR 420

Qy 447 DDFVEGLSFARSGGNWEECEFA 467
Db 421 DDFVEGLSFARSGGNWEECEFA 441

RESULT 4
US-09-121-425-2
; Sequence 2, Application US/09121425
; Patent No. 6153418
; GENERAL INFORMATION:

APPLICANT: Lehmann, Martin
TITLE OF INVENTION: Consensus Phytases
FILE REFERENCE: consensus phytases 13239
CURRENT APPLICATION NUMBER: US/09/121.425
CURRENT FILING DATE: 1998-07-23
EARLIER APPLICATION NUMBER: EPO 97112688.3
EARLIER FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 2

LENGTH: 467

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:consensus

OTHER INFORMATION: sequence

US-09-121-425-2

Query Match 88.0%; Score 2173; DB 3; Length 467;
Best Local Similarity 85.2%; Pred. No. 1.4e-220;
Matches 415; Conservative 13; Mismatches 19; Indels 40; Gaps 2;

Qy 1 MGVFVLLSLATIFGSGTALGPRGNHSCDVGGYOCFPEISHLWGQYSPFSLADE 60
Db 1 MGVFVLLSLATIFGSGTALGPRGNHSCDVGGYOCFPEISHLWGQYSPFSLADE 60
Qy 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKKYSALIEAQKNATAFKGYAFKLYN 120
Db 61 SAISPDVPDCCRVTFFQVLSRHGARYPTSSKKAYS-----TYN 100
Qy 121 YTLGADDLTPFEGQVNSGKIFRYRKALARKIVPFVRASGSDRVIASAEKFIQFQSA 180
Db 101 YTLGADDLTPFEGQVNSGKIFRYRKALARKIVPFIRASGSDRVIASAEKFIQFQSA 160
Qy 181 KLADPGANPHQASPVIN-----VIIPEGAGYNNLTLDHGLCTAFEE 220
Db 161 KLADPGSQHQAQSPVIDLIEAQKNATAFKGYAFKLYIPEGSGYNNLTLDHGLCTAFED 220
Qy 221 SELGDDVEANFTAFAPPFIRARLEAHLPGVNLTDDEVNLMDCPFDTVARTSDATQLSP 280
Db 221 SELGDDVEANFTALFAPAIRARLEADLPVLTDEDVYVLMDCPFETVARTSDATELSP 280
Qy 281 FCDLFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGVFNELIARLTHSPVQDHTSTNH 340
Db 281 FCALFTHDEWQYDYLQSLGKYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNH 340
Qy 341 TLDSNPATFPLNATLYADFSDHNTMYSIFFALGLYNGTKPLSTTSVESTTEEDGYAASWT 400
Db 341 TLDSNPATFPLNATLYADFSDHNSKISIFFALGLYNGTAPLSTTSVESTTEEDGYASWT 400
Qy 401 VPFAARAYVEMMOCEAEKPELVRVLVNDRVVPLHGGGVOKLGRCKRDDFVEGLSFARSGG 460
Db 401 VPFGARAYVEMMOCEAEKPELVRVLVNDRVVPLHGGCAVDKLGCRCKRDDFVEGLSFARSGG 460
Qy 461 NWEBCFA 467
Db 461 NWAECFA 467

RESULT 5

US-09-634-493A-2
Sequence 2, Application US/05634493A
Patent No. 6579975
GENERAL INFORMATION:
APPLICANT: Lehmann, Martin
TITLE OF INVENTION: Consensus Phytases
FILE REFERENCE: consensus phytases 13239
CURRENT APPLICATION NUMBER: US/09/634.493A
CURRENT FILING DATE: 2000-08-08
PRIOR APPLICATION NUMBER: US/09/121.425
PRIOR FILING DATE: 1998-07-23
PRIOR APPLICATION NUMBER: EPO 97112688.3
PRIOR FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 467
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:consensus
OTHER INFORMATION: sequence
US-09-634-493A-2

Query Match 88.0%; Score 2173; DB 4; Length 467;
Best Local Similarity 85.2%; Pred. No. 1.4e-220;
Matches 415; Conservative 13; Mismatches 19; Indels 40; Gaps 2;

Qy 1 MGVFVLLSLATIFGSGTALGPRGNHSCDVGGYOCFPEISHLWGQYSPFSLADE 60
Db 1 MGVFVLLSLATIFGSGTALGPRGNHSCDVGGYOCFPEISHLWGQYSPFSLADE 60
Qy 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKKYSALIEAQKNATAFKGYAFKLYN 120
Db 61 SAISPDVPDCCRVTFFQVLSRHGARYPTSSKKAYS-----TYN 100
Qy 121 YTLGADDLTPFEGQVNSGKIFRYRKALARKIVPFVRASGSDRVIASAEKFIQFQSA 180
Db 101 YTLGADDLTPFEGQVNSGKIFRYRKALARKIVPFIRASGSDRVIASAEKFIQFQSA 160
Qy 181 KLADPGANPHQASPVIN-----VIIPEGAGYNNLTLDHGLCTAFEE 220
Db 161 KLADPGSQHQAQSPVIDLIEAQKNATAFKGYAFKLYIPEGSGYNNLTLDHGLCTAFED 220
Qy 221 SELGDDVEANFTAFAPPFIRARLEAHLPGVNLTDDEVNLMDCPFDTVARTSDATQLSP 280
Db 221 SELGDDVEANFTALFAPAIRARLEADLPVLTDEDVYVLMDCPFETVARTSDATELSP 280
Qy 281 FCDLFTHDEWIOYDYLQSLGKYGYGAGNPLGPAQGVGVFNELIARLTHSPVQDHTSTNH 340
Db 281 FCALFTHDEWQYDYLQSLGKYGYGAGNPLGPAQGVGFANELIARLTRSPVQDHTSTNH 340
Qy 341 TLDSNPATFPLNATLYADFSDHNTMYSIFFALGLYNGTKPLSTTSVESTTEEDGYAASWT 400
Db 341 TLDSNPATFPLNATLYADFSDHNSMISIFFALGLYNGTAPLSTTSVESTTEEDGYASWT 400
Qy 401 VPFAARAYVEMMOCEAEKPELVRVLVNDRVVPLHGGGVOKLGRCKRDDFVEGLSFARSGG 460
Db 401 VPFGARAYVEMMOCEAEKPELVRVLVNDRVVPLHGGCAVDKLGCRCKRDDFVEGLSFARSGG 460
Qy 461 NWEBCFA 467
Db 461 NWAECFA 467

RESULT 6

US-08-868-435-33
Sequence 33, Application US/08868435
Patent No. 6291221
GENERAL INFORMATION:
APPLICANT: Van Loon, Adolphus
APPLICANT: Mitchell, David
TITLE OF INVENTION: POLYPEPTIDES WITH PHYLASE ACTIVITY
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: United States of America
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25


```

361 HNTMVSTFFALGLYNGTKPLSTTSVESIEETDGYAASWTVPFAARAYVEMMOCEAKEP 420
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
359 HONSMVSTFFALGLYNGTEPLSRSTSVEAKELDGYASASWVPEFGARAYFETMCKSEKEP 418
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347 LVRVLNDNRVPLHCCGVDKLGRCKRDDH*VEGLSFARSGGNWEECF 467
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
345 LVRVLNDNRVPLHCCGVDKLGRCKLND*VFKGLSNARSGGNWEECF 465
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RESULT 7
US-08-744-231-33
: Sequence 33, Application US/08744231
: Patent No. 6358722
: GENERAL INFORMATION:
: APPLICANT: Van Loon, Adolphus
: APPLICANT: Mitchell, David
: TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
: NUMBER OF SEQUENCES: 35
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Hoffmann-La Roche Inc.
: STREET: 340 Kingsland Street
: CITY: Nutley
: STATE: New Jersey
: COUNTRY: United States of America
: ZIP: 07110
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/744.231
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/424.757
: FILING DATE: 18-APR-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Kass, Alan P
: REGISTRATION NUMBER: 32142
: REFERENCE/DOCKET NUMBER: Case Docket 9339
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (201) 235-4205
: TELEFAX: (201) 235-2363
: INFORMATION FOR SEQ ID NO: 33:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 465 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 104
: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 119
: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 205
: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 228
: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 337
: OTHER INFORMATION: /note="potential N-glycosylation site"
: FEATURE:
: NAME/KEY: misc_feature

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; LOCATION: 374
; OTHER INFORMATION: /note="potential N-glycosylation site"
US-08-744-231-33

Query Match          77.0%; Score 1902; DB 4; Length 465;
Best Local Similarity 77.1%; Pred. No. 5.9e-192;
Matches 360; Conservative 37; Mismatches 68; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATLFGSTGALGPRGNSHSCDVTVDGGYQCFPEISHLWGQSPFFSLADE 6C
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MYTLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGQSPFFSLEDE 59

QY 61 SAISPDPVPGCRVTFVQVLSRHGARYPTSSSKSKYSALIEAIQKNATAFKGYAFLKTYN 22Q
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSSKSKYKLVTAIQANATDFKGFALKTYN 119

QY 121 YTLGADDLTPFGEQOMVNSGIKFYRYKALARKIVPVFRASGSDRVIASAEKFEQFQSA 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 120 YTLGADDLTPFGEQOMVNSGIKFYRYKALARKIVPVFRASGSDRVIASAEKFEQFQSA 179

QY 181 KLADPGANPHQASPVINVIIPGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 24C
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 180 KLADPGAT-NRAAPALSVILPESETFNNTLDHGVCIKFEASQLGDEVAANFTALFAPDIR 238

QY 241 ARLEAHLPGVNLTDDEVNLMDCPFDTVARTSDATQSLSPFCDLFTHDEWLOXYLQSLG 30Q
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 239 ARAEKHLPGVTITLDEVVSLMDMCSFDTVARTSDASQLSPFCQFTHNEMKKYQLQSLG 299

QY 301 KYGYGAGNPLGPAQGVGVNLIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 36C
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 299 KYGYGAGNPLGPAQGVGVNLIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 358

QY 361 HNTMYSIFFALGLYNGTKPLSTSVESIEETDGYAASWTVPFAARAYVENMGOEAEKEP 42Q
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 359 HNSMYSIFFALGLYNGTEPLSRTSVESAKELDGYASWVVPFGARAYFETMOCKSEKEP 418

QY 421 LVRVLNDRVPLHGCGVDKLGRCRDDPFVEGLSFARSGGNWECFA 467
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 419 LVRALINDRVPLHGCDVDKLGRCRLNDFVKLSWARSGGNWGECS 465

RESULT 8
US-09-044-718-78
; Sequence 78, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 78
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-78

Query Match          77.0%; Score 1902; DB 4; Length 465;
Best Local Similarity 77.1%; Pred. No. 5.9e-192;
Matches 360; Conservative 37; Mismatches 68; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATLFGSTGALGPRGNSHSCDVTVDGGYQCFPEISHLWGQSPFFSLADE 6C
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MYTLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGQSPFFSLEDE 59

; LOCATION: 374
; OTHER INFORMATION: /note="potential N-glycosylation site"
US-08-744-231-33

Query Match          77.0%; Score 1902; DB 4; Length 465;
Best Local Similarity 77.1%; Pred. No. 5.9e-192;
Matches 360; Conservative 37; Mismatches 68; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATLFGSTGALGPRGNSHSCDVTVDGGYQCFPEISHLWGQSPFFSLADE 6C
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MYTLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGQSPFFSLEDE 59
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QY 61 SAISPDPVPGCRVTFVQVLSRHGARYPTSSSKSKYSALIEAIQKNATAFKGYAFLKTYN 12Q
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSSKSKYKLVTAIQANATDFKGFALKTYN 119

QY 121 YTLGADDLTPFGEQOMVNSGIKFYRYKALARKIVPVFRASGSDRVIASAEKFEQFQSA 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 120 YTLGADDLTPFGEQOMVNSGIKFYRYKALARKIVPVFRASGSDRVIASAEKFEQFQSA 179

QY 181 KLADPGANPHQASPVINVIIPGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 24C
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 180 KLADPGAT-NRAAPALSVILPESETFNNTLDHGVCIKFEASQLGDEVAANFTALFAPDIR 238

QY 241 ARLEAHLPGVNLTDDEVNLMDCPFDTVARTSDATQSLSPFCDLFTHDEWLOXYLQSLG 30Q
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 239 ARAEKHLPGVTITLDEVVSLMDMCSFDTVARTSDASQLSPFCQFTHNEMKKYQLQSLG 299

QY 301 KYGYGAGNPLGPAQGVGVNLIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 36C
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 299 KYGYGAGNPLGPAQGVGVNLIARLTHSPVQDHTSTNHTLDSNPATFPLNATLYADFS 358

QY 361 HNTMYSIFFALGLYNGTKPLSTSVESIEETDGYAASWTVPFAARAYVENMGOEAEKEP 42Q
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 359 HNSMYSIFFALGLYNGTEPLSRTSVESAKELDGYASWVVPFGARAYFETMOCKSEKEP 418

QY 421 LVRVLNDRVPLHGCGVDKLGRCRDDPFVEGLSFARSGGNWECFA 467
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 419 LVRALINDRVPLHGCDVDKLGRCRLNDFVKLSWARSGGNWGECS 465

RESULT 9
US-09-636-499-6
; Sequence 6, Application US/09636499
; Patent No. 6475762
; GENERAL INFORMATION:
; APPLICANT: Stafford, Christian F.
; APPLICANT: Trinci, Anthony P.J.
; APPLICANT: Brookman, Jayne L.
; TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
; FILE REFERENCE: GC586-2
; CURRENT APPLICATION NUMBER: US/09/636,499
; CURRENT FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: US 60/148,960
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-636-499-6

Query Match          77.0%; Score 1902; DB 4; Length 465;
Best Local Similarity 77.1%; Pred. No. 5.9e-192;
Matches 360; Conservative 37; Mismatches 68; Indels 2; Gaps 2;

QY 1 MGVFVLLSIATLFGSTGALGPRGNSHSCDVTVDGGYQCFPEISHLWGQSPFFSLADE 6C
   ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MYTLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYQCSPATSHLWGQSPFFSLEDE 59

QY 61 SAISPDPVPGCRVTFVQVLSRHGARYPTSSSKSKYSALIEAIQKNATAFKGYAFLKTYN 12Q
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 60 LSVSSKLPKDCRITLVQVLSRHGARYPTSSSKSKYKLVTAIQANATDFKGFALKTYN 119

QY 121 YTLGADDLTPFGEQOMVNSGIKFYRYKALARKIVPVFRASGSDRVIASAEKFEQFQSA 180
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 120 YTLGADDLTPFGEQOMVNSGIKFYRYKALARKIVPVFRASGSDRVIASAEKFEQFQSA 179

QY 181 KLADPGANPHQASPVINVIIPGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 24Q
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 180 KLADPGAT-NRAAPALSVILPESETFNNTLDHGVCIKFEASQLGDEVAANFTALFAPDIR 238
```


RESULT 12

US-09-044-718-79

; Sequence 79, Application US/09044718

; Patent No. 6391605

; GENERAL INFORMATION:

; APPLICANT: KOSTREWA, Dirk

; APPLICANT: PASAMONTES, Luis

; APPLICANT: TOMSCHY, Andrea

; APPLICANT: van LOON, Adolphus

; APPLICANT: VOGEL, Kurt

; APPLICANT: WYSS, Markus

; TITLE OF INVENTION: MODIFIED PHYTASES

; FILE REFERENCE: Modified Phytases

; CURRENT APPLICATION NUMBER: US/09/044,718

; PRIOR FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: EP 97810175.6

; PRIOR FILING DATE: 1997-03-25

; NUMBER OF SEQ ID NOS: 82

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 79

; LENGTH: 465

; TYPE: PR1

; ORGANISM: Aspergillus fumigatus

US-09-044-718-79

Query Match 76.6%; Score 1893; DB 4; Length 465;

Best Local Similarity 76.9%; Pred. No. 5.3e-191;

Matches 359; Conservative 37; Mismatches 69; Indels 2; Gaps 2;

QY 1 MGVEVLLSTATLFGSTGTALPGRNHSCDVTGQYQCFPEISHLWGOYSPFFSLADE 60

DB 1 MVLTLFLLSAAYLLSGRVSAAPSSAG-SKSCDVTDLGYOCSPATSHLWGOYSPFFSLEDE 59

QY 61 SAISPDVPGKCRVTFQVLSRHGARYPTSSKKYSALIEAOKNATAFKGYAFKTYN 120

DB 60 LSVSSKLPKDCRITLVQLSRHGARYPTSSKKYKLVTAIQANATDFKGFAPFLKTYN 119

QY 121 YTLGADDLTPFGQOMVNSGKIFKRYKALARKIVPVFRASGSDRVIASAEKFIQFQSA 180

DB 120 YTLGADDLTPFGQOLVNSGKIFKRYKALARSVPVFRASGSDRVIASGEKFIQFOQA 179

QY 181 KLADPGANPHQASPVINIIPEGAGYNNTLDHGLCTAFEESELGDDVFANFTAVFAPTR 240

DB 180 KLADPGAT-NRAAPAISSVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238

QY 241 ARLEAHLPGVNLTDDEVNLMDCPDIVARTSDATOLSPFCDLFTDHWIYDYLQSLG 300

DB 239 ARAEKHLPGVTLTDEDVVSLLDMCSEDTVARTSDASQLSPFCOLFTHNEWKYNYIOSLG 298

QY 301 KYGYGAGNPLGPAQGVGVNELLIALTHSPVODHTSTNHTLDSNPATFPLNATLYADEFS 360

DB 299 KYGYGAGNPLGPAQGTGFTNELIALTRSPVODHTSTNHTLDSNPATFPLNATLYADEFS 358

QY 361 HONTMVSIFPFALGLYNGTKPLSTTSVFSIETDGYAASWTVPFAARAYVEMMOCEAEKEF 420

DB 359 HDNSMWSIFPFALGLYNGTEGLSRTSVESAKELDGYASVWVPFGARAYFETMOCKSEKEP 418

QY 421 LVRVLVNDRVVPLHGCGVDKLGRCRDKDFVEGLSFARSGNWECEFA 467

DB 419 LVRALINDRVVPLHGCDVDKLGRCKLNDVFKGLSWARSGNMGCEFS 465

RESULT 13

US-09-044-718-3

; Sequence 3, Application US/09044718

; Patent No. 6391605

; GENERAL INFORMATION:

; APPLICANT: KOSTREWA, Dirk

; APPLICANT: PASAMONTES, Luis

; APPLICANT: TOMSCHY, Andrea

; APPLICANT: van LOON, Adolphus

; APPLICANT: VOGEL, Kurt

; APPLICANT: WYSS, Markus

; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 439
; TYPE: PR1
; ORGANISM: Aspergillus fumigatus
US-09-044-718-3

Query Match 76.6%; Score 1892.5; DB 4; Length 439;
Best Local Similarity 80.0%; Pred. No. 5.4e-191;
Matches 352; Conservative 37; Mismatches 50; Indels 2; Gaps 1;

QY 28 SHSCDVTGQYQCFPEISHLWGOYSPFFSLADEKSAISPDVPGKCRVTFVCLSRHGARYP 87

DB 1 SKSCDVTDLGYOCSPATSHLWGOYSPFFSLEDELSVSSKLPKDCRITLVQVLSRHGARYP 60

QY 88 TSSKSKYSALIEAOKNATAFKGYAFKTYNLTGADDLTPFGQOMVNSGKIFKRY 147

DB 61 TSSKSKYKLVTAIQANATDFKGFAPLKYNYILGADDLTPFGQOLVNSGKIFKRY 120

QY 148 KALARKIVPVFRASGSDRVIASAEKFIQFQSAKLADPGANPHQASPVINIIPEGAGYN 207

DB 121 KALARSVPVFRASGSDRVIASGEKFIQFQSAKLADPGAT-NRAAPAISSVIIPESETFN 179

QY 208 NTLDHGLCTAFEESELGDDVFANFTAVFAPTRARLEAHLPGVNLTDDEVN:MDMCPD 267

DB 180 NTLDHGVCTFEASQLGDEVAANFTALFAPDIRAREKHLPGVTLTDEDVVSLLDMCSE 239

QY 268 TVARISDATOLSPFCDLFTDHWIYDYLQSLGKYGYGAGNPLGPAQGVGVNELLIALR 327

DB 240 TVARTSDASQLSPFCOLFTHNEWKYNYIOSLGKIFKRYGAGNPLGPAQGTGFTNELIALR 299

QY 328 THSPVODHTSTNHTLDSNPATFPLNATLYADESHDNTMVSIFPFALGLYNGTKPLSTTSVE 387

DB 300 TRSPVODHTSTNHTLDSNPATFPLNATLYADESHDNTMVSIFPFALGLYNGTKPLSTTSVE 359

QY 388 SIETDGYAASWTVPFAARAYVEMMOCEAEKEPLVRVLVNDRVVPLHGCGVDKLGRCRDK 447

DB 360 SAKELDGYASVWVPFGARAYFETMOCKSEKEPLVRALINDRVVPLHGCDVDKLGRCRCKLN 419

QY 448 DFVEGLSFARSGNWECEFA 467

DB 420 DFVKGLSWARSGNMGCEFS 439

RESULT 14

US-09-044-718-12

; Sequence 12, Application US/09044718

; Patent No. 6391605

; GENERAL INFORMATION:

; APPLICANT: KOSTREWA, Dirk

; APPLICANT: PASAMONTES, Luis

; APPLICANT: TOMSCHY, Andrea

; APPLICANT: van LOON, Adolphus

; APPLICANT: VOGEL, Kurt

; APPLICANT: WYSS, Markus

; TITLE OF INVENTION: MODIFIED PHYTASES

; FILE REFERENCE: Modified Phytases

; CURRENT APPLICATION NUMBER: US/09/044,718

; CURRENT FILING DATE: 1998-03-19

; PRIOR APPLICATION NUMBER: EP 97810175.6

; PRIOR FILING DATE: 1997-03-25

; NUMBER OF SEQ ID NOS: 82

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 12

; LENGTH: 449

; TYPE: PR1

ORGANISM: Aspergillus fumigatus
US-09-044-718-12

Query Match 76.6%; Score 1892.5; DB 4; Length 445;
Best Local Similarity 80.0%; Pred. No. 5.6e-191;
Matches 352; Conservative 37; Mismatches 50; Indels 1; Gaps 1;
QY 28 SHSCDRVGGYOCFFEISHLMGOYSPFFESIADESAISPDPVPGKCRVTFVQVLSRHGARYP 87
Db 11 SKSCOTVDLGYOCSPATSHLMGOYSPFFESLELSVSSKLPKDCRITLVQVLSRHGARYP 70
QY 88 TSKSCKKYSALIEATOKNATAPKGYAFKTYNTLTGADDLTPGEOMVNSGKIFYRY 147
Db 71 TSKSCKKYLKTAQANATDFKGFELKTYNTLTGADDLTPGEOMVNSGKIFYRY 130
QY 148 KALKARKIVFVRASSDRVVIASAEKFIIEGFSQAKLADPGANPHOASPVINVIPEGAGYN 207
Db 131 KALARSVWPFIRASGSDRVIASGENKFIIEGFSQAKLADPGAT-NRAAPAIISVIIPESETFN 189
QY 208 NTLDHGLCTAFEESELGDDVEANFTAVFAPPIRARELFAHLPGVNLIDEDVNLMDMCPFD 267
Db 190 NTLDHGVCTRFASQGLGDEVAANFTALFAPDIRAREKRLPGVTLTDEDVNLMDMCSFD 249
QY 268 TVARTSDATQLSPFCDLFTHDEWIOYDYLSGLGKYGYGAGNPLGPAOGVGFVNELIARL 327
Db 250 TVARTSDASQLSPFCOLFTHNEWKKYNTYLSGLGKYGYGAGNPLGPAOGIGFTNELIARL 309
QY 328 THSPVODHTSTNHTLDSNPATPLNATLYADFSHDNTMVSIFPAGLYNGTKPLSTTSVE 367
Db 310 TRSPVODHTSTNLTLSNPATPLNATHYVDFSHDMSVSIFFALGLNGTPELUSRTSVE 369
QY 388 SIETDGYAASWTVFPAARAYVEMMQCAEKEPLVRLVNDRVVPLHGGCGVDKLGCRKRD 447
Db 370 SAKELDGYASASWVVPFGARAYFETMQCKSEKPLVRLALINDRVVPLHGGCDVDKLGCRKLN 429
QY 448 DFVEGLSFARSGGNWEECEFA 467
Db 430 DFVKGLSWARSGGNWGECEFS 449

RESULT 15
US-09-044-718-81
; Sequence 81, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-09-044-718-81

Query Match 76.5%; Score 1890; DB 4; Length 465;
Best Local Similarity 76.7%; Pred. No. 1.1e-190;
Matches 358; Conservative 38; Mismatches 69; Indels 2; Gaps 2;
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Db 1 MVTITFLLSAAYLLSGEVSNAPSSAG-SKSCDTVDLGYOCSPATSHLMGOYSPFFSLEDE 59

QY 61 SAISPDVPKGRVTFVQVLSRHGARYPTSSKSKKYSALIEATOKNATAPKGYAFKTYN 120
Db 50 LSVSSKLPKDCRITLVQVLSRHGARYPTSSKSKKYLKTAQANATDFKGFELKTYN 119
QY 121 YTLGADDLTPGEOMVNSGKIFYRYKALARKIVFVRASGSDRVVIASAEKFIIEGFSQ 180
Db 120 YTLGADDLTAFEGEOLVNSGKIFYRYKALARSVWPFIRASGSDRVVIASGEKFIIEGFSQ 179
QY 181 KLAOPGANPHOASPVINVIPEGAGYNNTLDHGLCTAFEESELGDDVEANFTAVFAPPIR 240
Db 180 KLAOPGAT-NRAAPAIISVIIPESETFNNTLDHGVCTKFEASQLGDEVAANFTALFAPDIR 238
QY 241 ABLEAHLPGVNLIDEDVNLMDMCPFDTVARTSDATQLSPFCDLFTHDEWIOYDYLSGL 300
Db 239 ABRAKHLPGVTLTDEDVNLMDMCSFDTVARTSDASQLSPFCOLFTHNEWKKYNTYLSGL 298
QY 301 KYGYGAGNPLGPAOGVGFVNELIARLTHSPVODHTSTNHTLDSNPATPLNATLYADFS 360
Db 299 KYGYGAGNPLGPAOGIGFTNELIARLTHSPVODHTSTNLTLSNPATPLNATMYVDFS 358
QY 361 HDNTMVSIFPAGLYNGTKPLSTTSVESIETDGYAASWTVFPAARAYVEMMQCAEKEP 420
Db 359 HDNSHVSIFPAGLYNGTPELUSRTSVESAKELDGYASASWVVPFGARAYFETMQCKSEK 418
QY 421 LVRVLNDRVVPLHGGCGVDKLGCRKRDVFEGLSFARSGGNWEECEFA 467
Db 419 LVRALINDRVVPLHGGCDVDKLGCRKLNDFVKGLSWARSGGNWGECEFS 465

Search completed: October 3, 2003, 07:47:45
Job time : 14.9581 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: October 3, 2003, 07:48:21 : Search time 21.3866 Seconds
(without alignments)

5642.336 Million cell updates/sec

Title: US-09-488-265B-25

Perfect score: 2525
Sequence: 1 tatatgaattcattgagcgtg.....ttcgttaagaattcatata 1426

Scoring table:

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Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310856 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%

Maximum Match: 100%

Listing first 45 summaries

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-DB-Issued_Patents_AA -OPMT=fastan -SUFFIX=oct3.ra -MINMATCH=0.1 -LOCPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.ccdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-NO_WMAP -LARGEQUERY -NEC_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=180 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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Database : Issued_Patents_AA.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	2311	91.5	467	4 US-09-273-871A-9 Sequence 9, Appl
2	2185	86.5	441	3 US-09-121-425-1 Sequence 1, Appl
3	2185	86.5	441	3 US-09-634-493A-1 Sequence 1, Appl
4	2173	86.1	467	3 US-09-121-425-2 Sequence 2, Appl
5	2173	86.1	467	4 US-09-634-493A-2 Sequence 2, Appl
6	1902	75.3	465	3 US-08-868-435-33 Sequence 33, Appl
7	1902	75.3	465	4 US-08-744-231-33 Sequence 33, Appl
8	1902	75.3	465	4 US-09-044-718-78 Sequence 78, Appl
9	1902	75.3	465	4 US-09-636-499-6 Sequence 6, Appl
10	1902	75.3	465	4 US-09-273-871A-8 Sequence 8, Appl
11	1894	75.0	465	4 US-09-044-718-80 Sequence 80, Appl
12	1893	75.0	465	4 US-09-044-718-79 Sequence 79, Appl

13	1892.5	75.0	439	4	US-09-044-718-3	Sequence 3, Appl
14	1892.5	75.0	449	4	US-09-044-718-12	Sequence 12, Appl
15	1890	74.9	465	4	US-09-044-718-81	Sequence 81, Appl
16	1868	74.0	469	4	US-09-044-718-82	Sequence 82, Appl
17	1866	73.9	467	1	US-07-923-724-8	Sequence 8, Appl
18	1866	73.9	467	2	US-08-609-426A-8	Sequence 8, Appl
19	1866	73.9	467	2	US-08-374-652C-2	Sequence 2, Appl
20	1862	73.7	467	1	US-08-151-574-32	Sequence 20, Appl
21	1862	73.7	467	1	US-08-146-424-20	Sequence 20, Appl
22	1862	73.7	467	1	US-08-593-709-2	Sequence 2, Appl
23	1862	73.7	467	1	US-08-419-448-32	Sequence 32, Appl
24	1862	73.7	467	2	US-08-819-825-3	Sequence 3, Appl
25	1862	73.7	467	3	US-09-163-642-3	Sequence 3, Appl
26	1862	73.7	467	4	US-09-233-510-32	Sequence 32, Appl
27	1862	73.7	467	4	US-09-636-499-5	Sequence 5, Appl
28	1855	73.5	467	3	US-09-155-855-3	Sequence 3, Appl
29	1855	73.5	467	4	US-09-543-744-3	Sequence 3, Appl
30	1855	73.5	467	4	US-09-929-060-3	Sequence 3, Appl
31	1850	73.3	467	4	US-09-273-871A-11	Sequence 11, Appl
32	1843	73.0	462	4	US-09-636-499-12	Sequence 12, Appl
33	1841	72.9	466	3	US-08-868-435-12	Sequence 12, Appl
34	1841	72.9	466	3	US-08-744-231-12	Sequence 35, Appl
35	1826	72.3	466	3	US-08-868-435-35	Sequence 35, Appl
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37	1820	72.1	444	4	US-09-044-718-1	Sequence 1, Appl
38	1813.5	71.8	463	3	US-08-868-435-29	Sequence 29, Appl
39	1813.5	71.8	463	4	US-08-744-231-29	Sequence 29, Appl
40	1813.5	71.8	443	3	US-09-155-855-1	Sequence 1, Appl
41	1813	71.8	443	4	US-09-543-744-1	Sequence 1, Appl
42	1813	71.8	443	4	US-09-929-060-1	Sequence 1, Appl
43	1813	71.8	443	4	US-09-155-855-2	Sequence 2, Appl
44	1808	71.6	443	3	US-09-543-744-2	Sequence 2, Appl
45	1808	71.6	443	4	US-09-543-744-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-273-871A-9

Sequence 9, Application US/09273871A

Patent No. 6514495

GENERAL INFORMATION:

APPLICANT: Svendsen, Allan
TITLE OF INVENTION: Phytase Variants
FILE REFERENCE: 5618.500-US
CURRENT APPLICATION NUMBER: US/09/273.871A
CURRENT FILING DATE: 1999-03-22
PRIOR APPLICATION NUMBER: PA 1998 00407
PRIOR FILING DATE: 1998-03-23
PRIOR APPLICATION NUMBER: PA 1998 00806
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: PA 1998 01176
PRIOR FILING DATE: 1998-09-18
PRIOR APPLICATION NUMBER: PA 1999 00091
PRIOR FILING DATE: 1999-01-22
PRIOR APPLICATION NUMBER: 60/080.129
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/090.675
PRIOR FILING DATE: 1998-06-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 9

LENGTH: 467

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Variation

US-09-273-871A-9

Alignment Scores:

Pred. No.: 6.13e-212

Score: 2311.00

Percent Similarity: 95.93%

Length: 467

Matches: 435

Conservative: 13

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Best Local Similarity: 93.15%      Mismatches: 19
Query Match: 91.52%      Indels: 0
DB: 4      Gaps: 0
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QY 72 GCCTTGGGTCCTCGTGAATTCCTACTCTCTGACACTGTTGACGGTGGGTACCAATGT 131
DB 21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValASPGLYGLYTYRGInCys 40
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DB 41 PheProGluLeuSerHisLeuTrpGlyGlnItyrSerProTyrPheSerLeuGluASPGL 60
QY 192 TCTGCTATTTCTCCAGACGCTTCAAGGGTGTAGAGTTACTTTCGTTCAAGTTTGTCT 251
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QY 372 TACTTTGGTCTGACGACTTGACTCCATTGCGGTGAGACACAAATGTTAATCTCTGCT 431
DB 121 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 140
QY 432 ATTAAGTCTACAGAGATACAAGGCTTTGGCTAGAAAGATTGTTCCATTGCTAGAGCT 491
DB 141 IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 160
QY 492 TCTGGTCTCAGAGAGTTATTGCTTCTGCTGAAAGTTCATTGAAGGTTTCCATCTGCT 551
DB 161 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 180
QY 552 AAGTGGCTGACCCAGGTGCTAACCCACACACAGGCTTCTCCAGTTATTAAAGCTTTATT 611
DB 181 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspVal:LeuIle 200
QY 612 CCAGAGGCTGCTGTTACACACACACTTTGGACCGGTTTGTGTCGTTTCTGACGAA 671
DB 201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220
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DB 221 SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
QY 732 GCTAGATTGAAGCTCACTTGGCAGGTTTAACTTGACTGACGACGAGCGTTGTTAAGTTG 791
DB 241 AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu 260
QY 792 ATGACATGTGTCATTCGACACTGTGCTAGACTTCTGACGACTTCAATGTCGCA 851
DB 261 MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerIle 280
QY 852 TTTCTGCTGACTTGTCTACGACGAGTGAATTCATACGACTACTTGCATCTTGGGT 911
DB 281 PheCysAlaLeuPheThrHisAspGluTyrArgGluTyrAspTyrLeuGlnSerLeuGly 300
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DB 301 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAla 320
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QY 1332 TTGGGTAGATGTAAGACAGACGACTTCTGTTCAAGGTTTGTCTTTCGCTAGATCTGTTGGT 1391
DB 441 LeuGlyArgCysLysArgAspPheValGluGlyLeuSerPheAlaArgSerGlyGly 460
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RESULT 2
US-09-121-425-1
: Sequence 1, Application: US/09121425
: Patent No. 6153418
: GENERAL INFORMATION:
: APPLICANT: Lehmann, Martin
: TITLE OF INVENTION: Consensus Phylases
: FILE REFERENCE: consensus phylases 13239
: CURRENT APPLICATION NUMBER: US/09/121,425
: CURRENT FILING DATE: 1998-07-23
: EARLIER APPLICATION NUMBER: EPO 97112688.3
: EARLIER FILING DATE: 1997-07-24
: NUMBER OF SEQ ID NOS: 20
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 441
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence:consensus
US-09-121-425-1

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Percent Similarity: 95.69%      Conservative: 13
Best Local Similarity: 92.74%      Mismatches: 19
Query Match: 86.53%      Indels: 0
DB: 3      Gaps: 0

US-09-488-265B-25 (1-1426) x US-09-121-425-1 (1-441)

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QY 210 GTTCCAAAGGGTTAGAGTTACTTTCGTTTCAGTTTGTCTACACAGGTTGCTAGATAC 269
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QY	330	ACTGCTTTCAGGGTAACTAGCTAGCTTTCTTGAAGACTTACAACACTTTGGTGGCTGAC	389	QY	1410	GCT 1412	
Db	81	ThrAlaPheLysGlyLysAlaPheLeuLys:hrTyrAsnTyrThrLeuGlyLys:aaSp	100	Db	441	Ala 441	
QY	390	GACTTGCTCCATTCGGTGAACAAAGTGAAGTCTGCTAAGTCTCTACAGAAGA	449	RESULT: 3			
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Db	141	IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProG-y	160	: APPLICANT: Lehmann, Martin			
QY	570	GCTAACCCACACCAAGCTTCTCCAGTTATTAAAGTTATTATCCAGAAGTGGCTGTTAC	629	: TITLE OF INVENTION: Consensus Phytases			
Db	161	SerGlnProHisGlnAlaSerProValIleAspValIleIleProGluGlySerGlyTyr	180	: FILE REFERENCE: Consensus phytases 13239			
QY	630	RACACACTTTGGACACCGGTTTGTGACTGCTTCCGAAGATCTGAATGGCTGACGAC	699	: CURRENT APPLICATION NUMBER: US/09/634.493A			
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QY	690	STTGAAGCTAACTTCACTGCTGTTTGGCTCCACCTATTAGAGCTAGATGGAAGCTCAC	749	: PRIOR APPLICATION NUMBER: US/09/121.425			
Db	201	ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp	220	: PRIOR FILING DATE: 1998-07-23			
QY	750	TGCGAGGTATTACTGACTGACGACAGACGTTGTTAACTTGAITGACATGTTGCTCATC	809	: PRIOR FILING DATE: 1997-07-24			
Db	221	LeuProGlyValThrLeuThrAspGluAspValValTyrLeuMetAspMetCysProPhe	240	: NUMBER OF SEQ ID NOS: 20			
QY	810	GACACTGTTGCTAGAAGCTTCTGACGCTACTCAATTTGCTCCATTTCTGCTGCTGCT	869	: SOFTWARE: PatentIn Ver. 2.0			
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Db	361	GluSerIleGluGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg	380	Best Local Similarity: 92.74%			
QY	1230	GCTTACGTTGAATGATCAATGTGAAGCTCAAAAGCAACATTTGGTGTAGAGTTTGGTT	1289	Query Match: 86.53%			
Db	381	AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal	400	DB: 4			
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				Db 1 AsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCysPheProGluIleSerHis			
				QY 150 TTGCGGGTCAATACTCTCCATTTCTTCTTTGGCTCAGCAATCTGCTATTCTCCAGAC			
				Db 21 LeuTrpGlyGlnTyrSerProTyr:PheSerLeuGluAspGluSerAlaIleSerProAsp			
				QY 210 GTTCCAAAAGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCTAGACACGGTGTAGATAC			
				Db 41 ValProAspAspCysArgValThrPheValGlnValLeuSerArgHisGlyAlaArgTyr			
				QY 270 CCAACTTCTTAAAGTCTPAAAGTACTCTGCTTTGATTTGAAGCTATTCAAAAGACGCT			
				Db 61 ProThrSerSerLysSerLysAlaIyrSerAlaLeuIleGluAlaIleGlnLysAsnAla			
				QY 330 ACTGCTTTCAGGGTAACTAGCTAGCTTTCTTGAAGACTTACAACACTTTGGTGGCTGAC			
				Db 81 ThrAlaPheLysGlyLysAlaPheLeuLys:hrTyrAsnTyrThrLeuGlyAlaAsp			
				QY 390 GACTTGCTCCATTCGGTGAACAAAGTGAAGTCTGCTAAGTCTCTACAGAAGA			
				Db 101 AspLeuThrProPheGlyGluAsnGlnMetValAsnSerGlyLysPheTyrArgArg			
				QY 450 TACAAGGCTTTGGCTAGAAAGATTGCTCCATTGCTTGAAGCTTCTGCTGACAGAT			
				Db 121 TyrLysAlaLeuAlaArgLysIleValProPheIleArgAlaSerGlySerAspArgVal			
				QY 510 ATTGCTTCTGCTGAAGCTTCATTGAAGGTTTCCAACTCGCTAAGTGGCTACCCAGG			


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Db 141 IleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAlaLysLeuAlaAspProGly 160
QY 570 GCTAACCCACCAAGCTCTCCAGTTATTAAGCTATATTATTCACAGAGGTCCTGCTTAC 629
Db 161 SerGlnProHisGlnAlaSerProValIleAspValIleIleProGluGlySerGlyTyr 180
QY 630 AACACACTTTGACACACCGTTTGTACTGCTTTGGAAGAATCTGAATTTGGGTGACGAC 689
Db 181 AsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAspSerGluLeuGlyAspAsp 200
QY 690 GTTCAAGCTAACTCACTGCTGTTTCGCTCCACCTATTAGAGCTAGATTGGAAGCTCAC 749
Db 201 ValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArgAlaArgLeuGluAlaAsp 220
QY 750 TTGCAGGTGTTAACTGACTGACGAAGAGCTGTTTAAGTTGATGCAIGTGTCCATTC 809
Db 221 LeuProGlyValThrLeuThrAspGluAspValValThrLeuMetAspMetCysProPhe 240
QY 810 GACACTGTTGCTAGAACTTCTGACGCTACTCAATGCTCTCCATTCTGTGACTTGTACT 869
Db 241 GluThrValAlaArgThrSerAspAlaThrGluLeuSerProPheCysAlaLeuPheThr 260
QY 870 CACGACGAATGGATGTTCAATACGACTACTTGCATCTTTGGGTAAAGTACTACGTTACGGT 929
Db 261 HisAspGluThrArgGlnTyrAspTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGly 280
QY 930 GCTGGTAACCATTTGGTCCAGCTCAAGTGTGTTGTTTCGTTAAAGCAATTTGCTTACA 989
Db 281 AlaGlyAsnProLeuGlyProAlaGlnGlyValGlyPheAlaAsnGlnLeuIleAlaArg 300
QY 990 TTGACTCACTCTCCAGTTCAAGACCACTTCTTACTTAACCAACACTTTGACACTCAACCCA 1049
Db 301 LeuThrArgSerProValGlnAspHisThrSerThrAsnHisThrLeuAspSerAsnPro 320
QY 1050 GCTACTTCCGATGAAAGCTACTTTGCTAGCTGACTTCTCTCAGACACCACTAAGTT 1109
Db 321 AlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSerHisAspAsnSerMetIle 340
QY 1110 TCTATTTCTTCGCTTTGGGTTTGTACACAGGCTACTAAGCCATTGCTACTACTCTGTT 1169
Db 341 SerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAlaProLeuSerThrThrSerVal 360
QY 1170 GAATCTATTGAAGAACTGACGGTTACGCTGCTTCTTGACAGTCTCCATTCGCTGCTAGA 1229
Db 361 GluSerIleGluThrAspGlyTyrSerAlaSerTrpThrValProPheGlyAlaArg 380
QY 1230 GCTTACGTTGAATCATTCATGTAAGCTGAAAGCTGAAAGCAACCACTTGGTTAGAGTTTGGT 1289
Db 381 AlaTyrValGluMetMetGlnCysGlnAlaGluLysGluProLeuValArgValLeuVal 400
QY 1290 AACGACAGAGTTGTTCCATTCGACGGTTGTGGTTGTGACAAAGTTGGGTAGATGTAAGA 1349
Db 401 AsnAspArgValValProLeuHisGlyCysAlaValAspLysLeuGlyArgCysLysArg 420
QY 1350 GACGACTTGGTTGAAGGTTTGTCTTTCGCTAGATCTGTTGGTGAAGTGGGAAGAACTTTC 1409
Db 421 AspAspPheValGluGlyLeuSerPheAlaArgSerGlyGlyAsnTrpAlaGlnCysPhe 440
QY 1410 GCT 1412
Db 441 Ala 441
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RESULT 4

US-09-121-425-2

; Sequence 2, Application US/09121425

; Patent No. 6153418

; GENERAL INFORMATION:

; APPLICANT: Lehmann, Martin

; TITLE OF INVENTION: Consensus Phytases

; FILE REFERENCE: Consensus Phytases 13239

; CURRENT APPLICATION NUMBER: US/09/121.425

; CURRENT FILING DATE: 1998-07-23

; EARLIER APPLICATION NUMBER: EPO 97112688.3

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; EARLIER FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence
US-09-121-425-2
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Alignment Scores:

Pred. No.:	9,07e-199	Length:	467
Score:	2173.00	Matches:	415
Percent Similarity:	87.89%	Conservative:	13
Best Local Similarity:	85.22%	Mismatches:	19
Query Match:	86.06%	Indels:	40
DB:	3	Gaps:	2

US-09-488-265b-25 (1-1426) x US-09-121-425-2 (1-467)

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QY 12 ATGGCGGTGTTGCTGCTGCTACTGTCCATTGCTCCACTTGTTCGGTTCACATCGGTACC 71
Db 1 MetGlyValPheValValLeuLeuSerIleAlaThrLeuPheGlySerThrSerGlyThr 20
QY 72 GCCTTGGGTCTCGTGGTAATTCCTACTCTCTGTGACACGTGTGACGGTGTGTACCAATGT 131
Db 21 AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys 40
QY 132 TTCCCAAGAAATTTCTCAGCTTGTGGGTCAATCTCTCCATCTCTCTCTTTCGGCTGACGAA 191
Db 41 PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu 60
QY 192 TCTGCTATTCTCCAGACGTTCCAAAGGTTCTAGATTACITTCGTTCAAGTTTGTCT 251
Db 61 SerAlaIleSerProAspValProAspCysArgValThrPheValGlnValLeuSer 80
QY 252 AGACAGGTGCTAGATACCCAACTTCTTAAAGTCTAAGAAGTACTCTGCTTTGATTGAA 311
Db 81 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla----- 97
QY 312 GCTATTCAAAAGAACGCTACTGCTTTCAAGGTAAGTACGCTTCTTGAAGACHTTACAAC 371
Db 98 -----ThrTyrAsn 100
QY 372 TACACTTTGGGTGCTGACGACTTGACTCCATTCGGTGAACACAAATGGTTAACTCTGCT 431
Db 101 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluAsnGlnMetValAsnSerGly 120
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Db 121 IleLysPheTyrArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla 140
QY 492 TCTGGTTCGACAGCTTATTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 551
Db 141 SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla 160
QY 552 AAGTTGGTGAACGAGTCTAACCCACACCAAGGCTTCTCCAGTTATTAAC----- 602
Db 161 LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu 180
QY 603 -----GTTATTATT 611
Db 181 AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle 200
QY 612 CCAGAAGGTGCTGTTTACAAACACACTTTGGACCAAGGTTTGTGTACTGCTTTCGAAGAA 671
Db 201 ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp 220
QY 672 TCTGATTTGGTCAACGAGTGTGAGGTAAGTCACTTCACTGCTGCTGCTGCTGCTGCTGCT 731
Db 221 SerGluLeuGlyAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg 240
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QY	732	GCTAGATTGGAGCTCACTGCCAGGTGTTAACTTGACTGACGAGACGCTTGTAACTTG	791
Db	241	AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu	260
QY	792	ATGGACATGTGTCCACTCGACACACTGTTGCTAGAACTTCTGACGCTACTCAATGTTCTCCA	851
Db	261	MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrSerLeuSerPro	280
QY	852	TNCTGTGACTTGTTCACCTCAGCAGCAATGATTCATACGACTACTTGCATCTTTGGST	911
Db	281	PheCysAlaLeuPheThrHisAspGluTrpArgGlnTyrAspTyrLeuGlnSerLeuGly	300
QY	912	AAGTACTACGGTTAGGTGTGTAACCCATGTTGGTCCAGCTCAAGGTGTTCGTTTCGT	971
Db	301	LysTyrTyrGlyTyrGlyAlaGlyAspProLeuGlyProAlaGlnGlyValGlyPheAla	320
QY	972	AACGAATTGATTGCTAGACTGACCTCACTCTCCAGTTCAGACACACACITCTACTAACCAC	1031
Db	321	AsnGluLeuLeuAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnHis	340
QY	1032	ACTTTGGACTCTAACCCAGCTACTTCCCATTTGAAGCTACTTGTACGCTCACTCTCTC	1091
Db	341	ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer	360
QY	1092	CACGACACACTATGTGTTCTATTCTTCGCTTTGGGTTGTACAAACGGTACTAAGCA	1151
Db	361	HisAspAsnSerMetIleSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrAAsp	380
QY	1152	TGTGCTACTACTTCGTTGAATCTATTGAGAAACATGACGGTTACGCTGCTTCITGGAC	1211
Db	381	LeuSerThrThrSerValGluSerIleGluGluThrAspGlyTyrSerAlaSerIrpThr	400
QY	1212	GTTCCATTGCTGTGATGACTTACGTTGAAATGATGCATGTGAAGCTCAAAGGAACCA	1271
Db	401	ValProPheGlyAlaArgAlaTyrValGluMetMetGlnCysGlnAlaGluLysGluPro	420
QY	1272	TGTGTTAGAGTTTTGGTTAAGCAGACAGTTGTTCCATTCACCGGTTGTGGTGTTCACAG	1331
Db	421	LeuValArgValLeuValAsnAspArgValProLeuHisGlyCysAlaValAspLys	440
QY	1332	TTGGGTAGATGTAACAGACAGCACTTCGTTGAAAGGTTTGTCTTCGCTAGACTCGTGT	1391
Db	441	LeuGlyArgCysLysArgAspAspPheValGluGlyLeuSerPheAlaArgSerGlyCly	460
QY	1392	AACTGGGAAGAAITGTTTCGCT	1412
Db	461	AsnTrpAlaGluCysPheAla	467

RESULT 5

US-09-634-493A-2
: Sequence 2, Application US/09634493A

; Patent No. 6579975

; GENERAL INFORMATION:

APPLICANT: Lehmann, Martin

TITLE OF INVENTION: Consensus Phytases

FILE REFERENCE: consensus phytases 13239

CURRENT APPLICATION NUMBER: US/09/634,493A

CURRENT FILING DATE: 2000-08-08

PRIOR APPLICATION NUMBER: US/09/121,425

; PRIOR FILING DATE: 1998-07-23

; PRIOR PENDING DATE: 1998-07-29
; PRIOR APPLICATION NUMBER: EPO 97112688.3; PRIOR AFFILIATION NUMBER: EFO
; PRIOR FILING DATE: 1997-07-24; PRIOR FILING DATE: 1997
; NUMBER OF SEO ID NOS: 20; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0; SOF INAKE. F8
; SEO ID NO 2; SEQ ID NO 2
; LENGTH: 467

LENGTH: 100
TYPE: PR

ORGANISM: Artificial Sequence

ORGANISM:
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: consensus

OTHER INFORMATION:	DESCRIPTION:
OTHER INFORMATION:	SEQUENCE:

OTHER INFORMATION
US-09-634-493A-2

Alignment Scores:		
Pred. No.:	9, 07e-199	467
Score:	2173.0C	415
Percent Similarity:	87.89%	Conservative: 13
Best Local Similarity:	85.22%	Mismatches: 19
Query Match:	86.06%	Indels: 40
DR:	4	Gaps: 2

US-09-488-265B-25 (1-1426) x US-09-634-493A-2 (1-467)

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Qy	72	GCCTCGGGCCCTCGGTGAATTCACACTCTGTGACACGTGTGACGTGGTACCAATGT	131
Zb	21	AlaLeuGlyProArgGlyAsnSerHisSerCysAspThrValAspGlyGlyTyrGlnCys	40
Qy	132	TTCCAGAAATTTCTACACTGTGTGGGGCAATACTCTCCATCTCTTCCTTTTGGCTGACGAA	191
Db	41	PheProGluIleSerHisLeuTrpGlyGlnTyrSerProTyrPheSerLeuGluAspGlu	60
Qy	192	TCGTGCTATTTCCTCCAGACGCTCCAAAGGGTGTAGACGTACTTTCGTTCAAGTTTGTCT	251
Zb	61	SerAlaIleSerProAspValProAspCysArgValThrPheValGlnValLeuSer	80
Qy	252	AGACAGGGTGCTAGATACCCACTCTCTTAGTCTAAGAGTACTCTGCTTGTATGAA	311
Db	81	ArgHisGlyAlaArgTyrProThrSerSerLysSerLysAlaTyrSerAla	97
Qy	312	GCTATTCAAAGAACGCTACTGCTTTCAGGGTAAGTACGCTTCTTGAAGACTTCAAC	371
Db	98	-----ThrTyrAsn	100
Qy	372	TACACTTTGGGTGCTGACACTTGACTCCATTCGGTGAACAACAATAGTTACTCTGGT	431
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Qy	432	ATTAAGTCTACAGAAGATACAAAGCTTTGGCTACAAAGATTGTTCATTTCGTTAGAGCT	491
Db	121	IleLysPheTyrArgArgTyrLysAlaLeuAlaArgLysIleValProPheIleArgAla	140
Qy	492	TCGTGGTCTGACAGATTATTCGTCGCTGMAAGTTTCATTGAAGGTTTCCATCTGCT	551
Db	141	SerGlySerAspArgValIleAlaSerAlaGluLysPheIleGluGlyPheGlnSerAla	160
Qy	552	AAGTTGGCTGACCCAGGTGCTAACCCACCAAGCTCTCCAGTTATTAAAC	602
Db	161	LysLeuAlaAspProGlySerGlnProHisGlnAlaSerProValIleAspLeuIleGlu	180
Qy	603	-----GlnTyrTyr	611
Db	181	AlaIleGlnLysAsnAlaThrAlaPheLysGlyLysTyrAlaPheLeuLysValIleIle	200
Qy	612	CCAGAAGGTGCTGGTTACAAACAACACTTTGGACCAACGGTTGTACTGCTTTTCGAAGA	671
Db	201	ProGluGlySerGlyTyrAsnAsnThrLeuAspHisGlyThrCysThrAlaPheGluAsp	220
Qy	672	TCGTAATTTGGGTGACGAGCTGTGAACCTAACTTCACIGCTGTTCGCTCCACCTATTAGA	731
Zb	221	SerGluLeuGlyAspAspValGluAlaAsnPheThrAlaLeuPheAlaProAlaIleArg	240
Qy	732	GCTAGATTGGAAGCTCACCTTGCCAGGTGTTAACTTGACTGACGAAGACGTTGTTAACTTG	791
Db	241	AlaArgLeuGluAlaAspLeuProGlyValThrLeuThrAspGluAspValValTyrLeu	260
Qy	792	ATGGACATGTGCCATTGCACACTGTTGCTAGAACTTCTGACGCTACTCAATTGCTCCCA	851
Db	261	MetAspMetCysProPheGluThrValAlaArgThrSerAspAlaThrGluLeuSerPro	280
Qy	852	TTCTGTGACTTTGTTCTACTCACCAACAAATGGATTCAATACGACTACTTGCAAATCTTTGGGT	911

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Qy 1032 ACTTGGACTCTAACCCAGCTACTTCCCAATGAACGGTACTTTGTACGCTGACTTCCT 1031
Db 341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnAlaThrLeuTyrAlaAspPheSer 360
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RESULT 6
US-08-868-435-33
; Sequence 33, Application US/08868435
; Patent No. 6291221
; GENERAL INFORMATION:
; APPLICANT: Van Loon, Adolphus
; APPLICANT: Mitchell, David
; TITLE OF INVENTION: POLYPEPTIDES WITH PHYTASE ACTIVITY
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: United States of America
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/868,435
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/744,231
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kass, Alan P
; REGISTRATION NUMBER: 32142
; REFERENCE/DOCKET NUMBER: Case Docket 9339
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4205
; TELEFAX: (201) 235-2363

; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 465 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 104
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 119
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 205
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 228
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 337
; OTHER INFORMATION: /note="potential N-glycosylation site"
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 374
; OTHER INFORMATION: /note="potential N-glycosylation site"
; US-08-868-435-33
Alignment Scores:
Pred. No.: 6.6e-173 Length: 465
Score: 1902.00 Matches: 360
Percent Similarity: 85.01% Conservative: 37
Best Local Similarity: 77.09% Mismatches: 68
Query Match: 75.33% Indels: 2
DB: 3 Gaps: 2
US-09-488-265B-25 (1-1426) x US-08-868-435-33 (1-465)

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Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
Qy 72 GCCTTGGTCTCGTGTGTAATCTCCTCTTGTGACACTGTGTGACGGTGTACCAATGT 131
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
Qy 132 TTCCACAGAAATTTCTCCTCTTGTGGGTCAATCTCTCCATCTTCTCTTGTGGCTGACGAA 191
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
Qy 192 TCTGCTATTCTCCACAGCTTCCAAAGGGTTCAGAGTTACTTTCGTTCAAGTTCCTGTCT 251
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
Qy 252 AGACACGGCTAGATACCCAACTTCTTCTAAGTCTAAGAGTACTCTGCTTTCGATGAA 311
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysTyrLysLeuValThr 99
Qy 312 GCTATTCAAAGNACGCTACTGCTTTCAGGGTAGTACGCTTCTTCAAGACTTCAAC 371
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
Qy 372 TACACTTTGGGTGCTCAGCAGCTTGTACTCCATTCGGTGAACAAATGTTAACTCTGGI 431
Db 120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
Qy 432 ATTAAGTTCTACAGAGATACAGGCTTTGGCTAGAAAGATTTGCTTCCATTCCTAGACT 491
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159


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QY 132 TTCCACAGAAATTTCTCACTGTGGGGTCAATACCTCCATCTCTCTCTTTGGCGAGAA 192
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 40 SerProAlaIleThrSerHisLeuTrpGlyGlnTrpSerProPhePheSerLeuGluAspGlu 59
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DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 80 ArgHisGlyAlaArgTyProThrSerSerLysSerLysTyLysLysLeuValThr 99
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QY 372 TACACTTTGGGTGCTGACGACTTGACTCCATTCCTGCTGAGTGAACCAACAATGGTTACTCTGGT 431
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 432 ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAGATTGTTCCATTCGTTAGAGCT 491
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 140 IleLysPheTyGlnArgTyLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 492 TCTGTTCTGACAGAGTTATTCCTTCTGCTGAAAGTTCATTTGAAGTTTCCATCTGCT 551
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGlyPheGlnGlnAla 179
QY 552 AAGTTGGTGTACCCAGGTGTAACCCACCAACCACTTCCTCCAGTTATTAAGTTATTATT 611
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 196
QY 612 CCAGAAGGTCGTGTACACACACTTTGCACACAGGTTGTTGCTACTGCTTTCGAGAA 671
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 672 TCTGAATTTGGGTGACGAGTGTGAAGCTTAACCTCACTGCTGTTTTCGCTCCACCTATTAGA 731
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 236
QY 732 GCTAGATTGGAAGCTCACTTGCACGTTGTTAACTTGACTGACGAAGAGCTGTGTTAATG 791
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 239 AlaArgAlaGluHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 792 ATGGACATGTCTCCATTCGACACTGCTGTAAGACTTCTGACGCTACTCAATTCCTCCA 851
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DB 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 276
QY 852 TTCTGTGACTTGTCTCACTCACAGCAATGGATTCAATACGACTACTTGCATCTTTGGGT 911
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 279 PheCysGlnLeuPheThrHisAsnGlnTrpLysTyLysTyLysAsnTyLysLeuGlnSerLeuGly 298
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DB 299 LysTyTyTyGlyTyGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 316
QY 972 AAGCAATGATTGCTAGATTGACTCTCCAGTTCAGAGTCAAGACCACTCTCTACTAAACAC 1031
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DB 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1032 ACTTTGGACTCTAACCCAGCTACTTTCCTTGAAGCGTACTTTGACGCTGACTTCTCT 1091
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DB 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyValAspPheSer 358
QY 1092 CAGCAACACTATGTTCTATTCTTCTGCTTGGGTTGTCAACGGGTACTAAAGCCA 1151
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DB 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyAsnGlyThrGluPro 378
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RESULT 8

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US-09-044-718-78
: Sequence 78, Application US/09044718
: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTRENA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044.718
: PRIOR FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: Patent Ver. 2.1
: SEQ ID NO 78
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-09-044-718-78
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Alignment Scores:
Pred. No.: 6,6e-173 Length: 465
Score: 1902.00 Matches: 360
Percent Similarity: 85.01% Conservative: 37
Best Local Similarity: 77.09% Mismatches: 68
Query Match: 75.33% Indels: 2
DB: 4 Gaps: 2
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US-09-488-265b-25 (1-1426) x US-09-044-718-78 (1-465)

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QY 12 ATGGCGCTGTTCTGCTGCTACTGCTCAATTCACCTTTCGCTTCCACATCCGGTACC 71
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 1 MetValThrLeuThrPheLeuLeuSerAlaAlaThrLeuLeuSerGlyArgValSerAla 20
QY 72 GCCTTGGGTCTCGTGGGTAAATTCACCTTCACCTGTTGACAGCTGTTGACGGTGTACCAA 131
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyGlnCys 39
QY 132 TTCCACAGAAATTTCTCACTTGTGGGGTCAATACCTCTCCATCTCTCTTTGGCTGACGAA 191
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 40 SerProAlaThrSerHisLeuTrpGlyGlnTrpSerProPhePheSerLeuGluAspGlu 59
QY 192 TCTGTTATTTCTCCACAGAGTTCCAAAGGGTTGTAAGATTACTTTCGTTCAAGTTTGTCT 251
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 252 AGACACGGTGTGTAGATACCAACTCTTCTAAGTCTTGAAGAGTACTCTGCTTGTGATTGAA 311
DB 111 111 111 111 111 111 111 111 111 111 111 111 111 111 111
DB 80 ArgHisGlyAlaArgTyProThrSerSerLysSerLysTyLysLysLeuValThr 99
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QY 312 GCTATTCAAAAGACCTACTGCTTTCAGGGTAAGTACGCTTCTTGAAGACTTACAAAC 371
DB 100 AAlleGlnAlaAsnAlaThrAspPheTyrGlySerPheAlaPheLeuLysThrTyrAsn 119
QY 372 TACACTTGGTGCTGACGACTGACTCCATTCCGTTGGAACAACAATGGTTAACTCTGCT 431
DB 120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 432 ATTAAGTTCTACAGAAGAACAAGGTTTGGCTAGAAAGATTGTTCCATTCTGTTAGACT 491
DB 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 492 TCTGGTCTGACAGAGTTATTGCTTCGCTGAAAGAGTTCATTGAAGGTTTCCAATCTGCT 551
DB 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAla 179
QY 552 AAGTTGGCTGACCCAGGCTGAACCCACACCAAGCTTCGCCAGTTATTAAAGTTATTAT 611
DB 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
QY 612 CGAAGAGTGCTGGTTACACAAACACTTTGGACCAGGTTTGTGTACGCTTTCGAAGAA 571
DB 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 216
QY 672 TCTGAATTGGTGACGACCTTGAAGCTAACTTCACTGCTGCTGTTTCGCTCCACCTAT 731
DB 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 236
QY 732 GTAGATTGGAGCTCAGCTTGCAGGTGTTAACTTACCTGACGACGAGAGGTTGTTAACT 751
DB 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 792 ATGGACATGTGCTCCATTCACACACTGTTGCTAGAACTTCTGACGCTACTCAATTGCT 851
DB 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 852 TTCTGTGACTTGTTCACCTCAGCAGAACTGATTCATACGACTACTTGCATCTTGTGGT 911
DB 279 PheCysGlnLeuPheThrHisAsnGluTrpLysTyrAsnTyrLeuGlnSerLeuGly 296
QY 912 AGTACTACGGTTACGGTCTGCTTAACCCATTGGGTCCAGCTCAAGGTGTGGTTCTGTT 971
DB 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 972 AAGCAATTGATTGCTAGATTGACTCCTCCAGTTCAGACACCACTCTACTAACCAC 1031
DB 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1032 ACTTTGGACTCTAACCACGCTACTTCCCATTTGAACGCTACTTTGTACGCTACTCTCT 1092
DB 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1092 CAGCACAACACTATGTTCTATTCTTCCTGTTGGGTTTGTACACGGTACTTAAGCCA 1151
DB 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 376
QY 1152 TTCTCTACTACTTCTGTTGAATCTATGAAAGAACTGACGGTTACGCTGCTTCTTGGACT 1211
DB 379 LeuSerArgThrSerValGluSerAlaTyrGluLeuAspGlyTyrSerAlaSerTrpVal 396
QY 1212 GTTCCATTGCTGCTAGAGCTTACGTTGAATGATGCAATGTGAGAGCTGAAAGGAACA 1271
DB 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGlyLysGluPro 418
QY 1272 TTGTTTAGAGTTTGGTTAAACGACAGAGTTGTCCATTGCACGGTTGGTGTTCACAG 1331
DB 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 436
QY 1332 TTGGGTAGATTGAAGAGAGACACTTCTGTTGAAGTTTGTCTTCCTAGATCTGGTGT 1391
DB 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
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QY 1392 AACTGGGAAGATGTTTCGCT 1412
DB 459 AsnTrpGlyGluCysPheSer 465
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PESULT 9
US-09-636-499-6
: Sequence 6, Application US/09636499
: Patent No. 6475762
: GENERAL INFORMATION:
: APPLICANT: Stafford, Christian F.
: APPLICANT: Trinci, Anthony P.J.
: APPLICANT: Brookman, Jayne L.
: TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
: TITLE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating Sa
: FILE REFERENCE: GC586-2
: CURRENT APPLICATION NUMBER: US/09/636,499
: PRIOR APPLICATION NUMBER: 2000-08-11
: PRIOR FILING DATE: 1999-08-13
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 465
: TYPE: PR1
: ORGANISM: Aspergillus fumigatus
US-09-636-499-6
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Alignment Scores: 6.4e-173 Length: 465
Pred. NO.: 1902.00 Matches: 360
Score: 1902.00 Conservative: 37
Percent Similarity: 85.01% Mismatches: 66
Best Local Similarity: 77.09% Indels: 2
Query Match: 75.33% Gaps: 2
DB: 4

US-09-488-265B-25 (1-1426) x US-09-636-499-6 (1-465)
QY 12 ATGGCGCTGTTGCTGCGTACTGTCGATTCGACCTGTTGGTTCCACATCCGCTACC 71
DB 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 72 GCCTTGGGTCCTCGTGGTAAATCTCCTCTTTGTCACACTGTTGACGGTGTACCAATGT 131
DB 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 132 TTCACAAATTTTCACCTTGTGGGTCAATAGTCTCCATCTCTCTTGGCTGACGAA 191
DB 40 SerProAlaThrSerHisLeuTrpGlyLysTyrSerProPheSerLeuGluAspGlu 59
QY 192 TCTGCTATTTCTCCAGACGTTCCAAAGGGTGTAGAGTTACTTTCGTTCAAGTTTGTCT 251
DB 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 252 AGACACGGTCTAGATACCCACTTCTTCTAAGTCTAAGAGTACTGCTTGTGATTGAA 311
DB 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysLysLysLysLysLys 99
QY 312 GCTATTCAAAAGACGCTACTGCTTTCAAGGGTAAGTACGCTTCTTGAAGACTTACAA 371
DB 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 372 TACACTTGGGTCGTGACGACTTGCATTCGCTCCATTCCGTTGGAACAACAATGGTTAACTCTGCT 431
DB 120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 432 ATTAAGTTCTACAGAAGTTCGCTTTCGCTAGAAAGATTGTTCCATTCTGTTAGACT 491
DB 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 492 TCTGGTCTGACAGAGTTATTGCTTGTGCTGAAAGTTCATTCGAAGTTTCCAATCTGCT 551
DB 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
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QY 612 CCAGAGGCTGCTGGTTACACACACTTTGGACCAGGTTTGTGTACTGCTTTCCAGAA 671
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 672 TCTCAATTGGGTGACAGCTTGAAGCTAATCTCACTGCTGCTTTCCGCTCCACCTATAGA 731
Db 219 SerGluLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 732 GCTAGATTGGAAGCTCAGCTGCCAGGTGTTAACTTGAAGTGAAGAGAGCTTGTAACTTG 791
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 792 ATGGACATGTGTCATTCGACACTGTTGCTAGAACTTCTGAGCTTCTGAGCTTCAATTTGCTCCA 851
Db 259 MetAspMetCysSerPheAspThrValAlaAlaArgThrSerAspAlaSerGluLeuSerPro 278
QY 852 TCTGTGAGCTTGTTCACCTCAGCAGCAATGATTCAATAGCAGCTACTTGCATCTTGGGI 911
Db 279 PheCysGluLeuPheThrHisAsnGluThrLysLysTyrrAsnThrLeuGluSerLeuGly 298
QY 912 AAGTACTACGGTTACGGTGCTGCTAACCCATTGGTCCAGCTCAAGGTGTTGTTTCGTT 971
Db 299 LysTyrrGlyTyrrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyLeGlyPheThr 318
QY 972 AAGCAATTGATGCTAGATTGACTCAGCTCTCCAGTTCAGAGCCACACTTCTACTAACCCAC 1031
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QY 1092 CAGCAGCAACTATGTTCTTCTTCTTCGCTTGGTTGGTTGTAGACGGTACTAGCCCA 1151
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrrAsnGlyThrGluPro 378
QY 1152 TTCTCTACTACTTCTTTGAATCTATTTGAAGAACTGACGGTTAGCTGCTTCTTGGACT 1211
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QY 1212 GTCCATTCGCTGCTAGACCTTACGTTGAATGTGCAATGTGAGCTGGAAGCAAGCA 1271
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QY 1272 TTGGTTAGAGTTTGGTTAACGACAGAGTTGTTCCATTGCACGGTTGGTGTTCACAG 1331
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY 1332 TTGGTTAGATGTAAAGACAGACACTTCGTTGAAGTTTGTCTTTCGCTAGATCTGGTGT 1391
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerIrpAlaArgSerGlyGly 458
QY 1392 AACTGGGAAGATGTTTCGCT 1412
Db 459 AsnTrpGlyGluCysPheSer 465
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RESULT 10

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US-09-273-871A-8
: Sequence 8, Application US/09273871A
: Patent No. 6514495
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: TITLE OF INVENTION: Phytase Variants
: FILE REFERENCE: 5618.500-US
: CURRENT APPLICATION NUMBER: US/09/273.871A
: CURRENT FILING DATE: 1999-03-22
: PRIOR APPLICATION NUMBER: PA 1998 00407
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: PA 1998 00806
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: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: PA 1998 61176
: PRIOR FILING DATE: 1998-09-18
: PRIOR APPLICATION NUMBER: PA 1999 00091
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/090,129
: PRIOR FILING DATE: 1998-03-31
: PRIOR APPLICATION NUMBER: 60/090,675
: PRIOR FILING DATE: 1998-06-25
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 8
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: LENGTH: 465
: TYPE: PRI
: ORGANISM: Aspergillus fumigatus
US-09-273-871A-8
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Alignment Scores:

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Seq. No.: 6,6e-173 Length: 465
Score: 1902.00 Matches: 360
Percent Similarity: 85.01% Conservative: 37
Best Local Similarity: 77.09% Mismatches: 68
Query Match: 75.33% Indels: 2
DB: 4 Gaps: 2
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US-09-488-265B-25 (1-1426) x US-09-273-871A-8 (1-465)

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QY 12 ATGGCGGTGTCGTGCTGCTAGCTGCTCCACTTCCACCTTCTCGGTTCACATCCGGTACC 71
Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaThrLeuLeuSerGlyArgValSerAla 20
QY 72 GCGTGGGTCCCTCGTGGTAATTCCTCACTTCTGTCACACTGTCAGCGTGGTGTACCAATGT 131
Db 21 AlaProSerSerAlaGly ---SerLysSerCysAspThrValAspLeuGlyTyrrGlnCys 39
QY 132 TTCCAGAAATTCCTCACTTGGGTGCAATCTCCATCTCCCTCTCTGCTGCTCAGCA 191
Db 40 SerProAlaThrSerHisLeuThrGlyGlnThrValSerProPhePheSerLeuGluAspGlu 59
QY 192 TCTGCTATTCTCCAGACAGCTTCCAAAGGTTGTAGAGTTACTTTCGTTCAAGTTTGTCT 251
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 252 AGACACGGTGTAGATACCCACTTCTCTCACTTCTAGCTTAAGAGTACTGCTGTGATTGAA 311
Db 80 ArgHisGlyValArgTyrrProThrSerSerLysSerLysIleValLysLysLeuValThr 99
QY 312 GCTATTCAAAAAGAACGCTACTGCTTCAAGGTAAGTACGCTTCTTCAAGACTTACAAC 372
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrrAsn 129
QY 372 TACACTTGGTGTGCTGACGACTTGACTTCATTCGCTGGTGAAACAAATGGTTAACTCTGGI 431
Db 120 TyrThrLeuGlyValAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 432 ATTAAGTCTTACAGAGATACAAAGCTTTGGCTACAAAGATTGTTCATCTGTTAGAGCT 491
Db 240 IleLysPheTyrrGlnArgTyrrLysAlaLeuAlaArgSerValValPropheIleArgAla 159
QY 492 TCTGGTTCTGACAGAGTTATTGCTTCTGCTGAAAAGTTCAATTGAAGTTTCCAATCGCT 551
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGluAla 179
QY 552 AAGTTGGCTGACCCAGGTGCTTAACCCACACCAAGCTTCTCCAGTTATTAAAGTTATTATT 611
Db 180 LysLeuAlaAspProGlyAlaThr ---AsnArgAlaAlaProAlaIleSerValIleLe 198
QY 612 CCAGAAAGTGTGCTGTTTACAAACACACTTGGACCCAGCTTGTGTGCTACTGCTTCCAGAA 671
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 672 TCTGAATTGGGTGACAGCTTGAAGCTAACTTCACTGCTGTTTTCGCTCCACCTATTAGA 731
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
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299	LYSYTYRGLYTYRGLYALAGLYASNPROLEUGLYPROALAGLNGLYILSGLYPHETHR	318
972	AACGAATTGATTGCTAGATCACTCACTCTCCAGTTCAAGACACACACTCTACTAACCA	1531
319	ASNGLULEUILLALAAQLAUThrASYSerPROValGLUAspHisThrSerThrAsnSer	338
1032	ACTTTGGACTCAACCCAGCTACTTCCCATTTGAACGCTACTTCTACGCTGACTCTCT	1091
339	ThrLeuValSerAsnPROAlaThrPheProLeuAsnAlaThrMetIlyValAspPheSer	358
1092	CACGACAACTACTATGGTTTCTATTTCTTCGCTTTGCGTTGTGACACGGTCACTAA	1151
359	HISAspAsnSerMetValSerIIEPhePheAlaLeuGLYLeuTYrAsnGLYThrGL	378
1152	TGTGCTACTACTCTGTGTGAATCTATTGAAGAACTGACGGTTACGCTGCTTC	1211
379	LeuSerArgThrSerValGLUSeRALaLYSGLULeuAspGLYTYrSerAlaSerTrpVal	396
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399	ValProPheGLYAlaArgAlaTYrPheGLUInrMetGlnCYSYSerGLULYSGLUSe	419
1272	TGTGTTAGAGTTTGTGGTTAACGACAGAGTTGTTCACITGCACGGTGTGTGTGACA	1331
419	LeuValArgAlaLeuIIEAsnAspAValValProLeuHisGLYCYSAspValAspLYS	436
1332	TGTGGTACATCTAAGACAGCACTTCGTTGTGAAGCTTCTCTTCGCTAGACTGGT	1391
439	LeuGLYArgCYSLYSLeuAsnAppPheValLYSGLYLeuSerTrpAlaArgSerGLYGLY	456
1392	AACTGGGAAGAAATGTTTCGCT	1412
459	AsnTrpGLYGLUCYSYPheSer	465

RESULT 12

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US-09-044-718-79
; Sequence 79, Application US/09044718
; Patent No. 6391605
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/09/044,718
; CURRENT FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 465
; TYPE: PRI
; ORGANISM: Aspergillus fumigatus
US-09-044-718-79

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Alignment Scores:	
Pred. No.:	4,77e-172
Score:	1893.00
Percent Similarity:	84.80%
Best Local Similarity:	76.87%
Query Match:	74.97%
DB:	4
	Indels: 2
	Gaps: 2
	Mismatches: 69
	Conservative:
	Matches: 359
	Length: 465

US-09-488-265B-25 (1-1426) x US-09-044-718-79 (1-465)

QY	12	ATGGGCGTGTCGTCTACTGTGCATTGCCACCTGTTCCGTTCCACATCCGGTACC	7:
Db	1	MetValThrLeuThrPheCLeuSeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla	20


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: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: CURRENT FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 12
: LENGTH: 449
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-09-044-718-12

Alignment Scores:
Pred. No.: 5,21e-172 Length: 449
Score: 1892.50 Matches: 352
Percent Similarity: 88.41% Conservative: 37
Best Local Similarity: 80.00% Mismatches: 50
Query Match: 74.95% Indels: 1
DB: 4 Gaps: 1

US-09-488-265b-25 (1-1426) x US-09-044-718-12 (1-449)

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QY 153 TGGGGTCAATCTCCATCTCTCTCTTGGGTGAGCAATCTGCTATTTCTCCAGACTT 212
DB 31 TrpGlyGlnTyrSerProPheSerLeuGluAspGluLeuSerValSerLysLeu 50
QY 213 CCAAGGGTGTAGAGTACTTCTGCTCAAGTTTCTGCTAGACAGGCTGCTAGACGCA 272
DB 51 ProLysAspCysA-GlleThrLeuValGlnValLeuSerArgHisGlyAlaArgTyrPro 70
QY 273 ACTTCTCTAGCTCAGACAGTACTCTGCTTTCGATGAGCAATTCATCAAAAGACGCTACT 332
DB 71 ThrSerSerLysSerLysLysTyrLysLysLeuValThrAlaIleGlnAlaAsnAlaThr 90
QY 333 GCTTTCAGGGTAAAGTACGCTTCTTCAAGACTTACAACTACACTTTGGTCTGACGAC 392
DB 51 AspPheLysGlyLysPheAlaPheLeuLysThrTyrAsnTyrThrLeuGlyAlaAspAsp 110
QY 393 TTGACTCCATTCGGTGAACACAAATGGTTAACTCTGGTATTAAAGTTCTACAGACATAC 452
DB 111 LeuThrProPheGlyGlnGlnGlnLeuValAsnSerGlyIleLysPheTyrGlnArgTyr 130
QY 453 AAGGCTTGGCTAGAAAGATTGTTCCATTCTGCTAGAGCTTCTGGTCTGACAGAGTTAT 512
DB 131 LysAlaLeuAlaArgSerValValProPheIleArgAlaSerGlySerAspArgValIle 150
QY 513 GCTTCTGCTGAAAAGTTCAITGAGGTTTCCCAATCTGCTAAAGTTGGCTGACCCAGCTGCT 572
DB 151 AlaSerGlyGluLysPheIleGluGlyPheGlnGlnAlaLysLeuAlaAspProGlyAla 170
QY 573 RACCCACACCAAGGTTCTCCAGTTATTAAAGTTATTATTCACAGAGGCTGCTGTTACAC 632
DB 171 Thr---AsnArgAlaAlaProAlaIleSerValIleIleProGluSerGluThrPheAsn 189
QY 633 AACACTTTGGACCGGTTTGTGCTACTGCTTTCCGAAGATCTCAATTTGGGTGACGACGCTT 692
DB 190 AsnThrLeuAspHisGlyValCysThrLysPheGluAlaSerGlnLeuGlyAspGluVal 209
QY 693 GAAGCTAACTTCACTGCTGTTTCGCTCCACCTATTAGACGTAGATTGGAAGCTCACTTG 752

210 AlaAlaAsnProThrAlaLeuPheAlaProAspIleArgAlaArgAlaGlyLysHisLeu 229
753 CCAGGTGTAAGTCTGACCTGACCAACACGTTTCTTAACTTGAATGACATGCTGCTCATTCGAC 812
230 ProGlyValThrLeuThrAspGluAspValValSerLeuMetAspMetCysSerPheAsp 249
813 ACTGTTGCTAGAACTTCTGACGCTACTCAATGTCTCCATCTGCTGACTGCTTCTCACTAC 872
250 ThrValAlaArgThrSerAspAlaSerGlnLeuSerProPheCysGlnLeuPheThrHis 269
873 GACGAATGATTCATACGACACTTCTGCAATCTTTGGGTAAAGTAACTACGCTTACGGTGT 932
270 AsnGluTyrLysLysTyrAsnTyrLeuGlnSerLeuGlyLysTyrTyrGlyTyrGlyAla 289
933 GGTAACCCATTGGGTCCAGCTCAAGGTGTTGGTTTCTTAAACGAATGATGCTAGATG 992
290 GlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThrAsnGluLeuIleAlaArgLeu 309
993 ACTCACTCTCCAGTTCAAGACACACTTCTACTACCCACACTTTGGACTCTACCCAGCT 1052
310 ThrArgSerProValGlnAspHisThrSerThrAsnSerThrLeuValSerAsnProAla 329
1053 ACTTTCCCATTCGAACGCTACTTGTACGCTGACTTCTCTCAGCACAACACTATGGTTTCT 1112
330 ThrPheProLeuAsnAlaThrMetTyrValAspPheSerHisAspAsnSerMetValSer 349
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1173 TCTATTGAAGAACTGACGGTTTACGCTCTTCTTGGACTGTTCTCATTCGCTGCTAGAGCT 1232
370 SerAlaLysGluLeuAspGlyTyrSerAlaSerThrValValProPheGlyAlaArgAla 389
1233 TAGCTTGAATGATGCAATGTGAAGCTGAAAAGAACCATTTGGTTAGAGTTTGGTTTAA 1292
390 TyrPheGluThrMetGlnCysLysSerGluLysGluProLeuValArgAlaLeuIleAsn 409
1293 GACAGAGTTGTTCCATTGACGGTTGCTGCTTTCACAGTGGGTAGATGTAAGAGAGAC 1352
410 AspArgValValProLeuHisGlyCysAspValAspLysLeuGlyArgCysLysLeuAsn 429
1353 GACTTCGTTGAGGTTTGTCTTTCGCTAGATCTGCTGTAAGTCTGGGAAGAAATGTTTCGCT 1412
430 AspPheValLysGlyLeuSerThrAlaArgSerGlyCysAsnTyrGlyGluCysPheSer 449

RESULT 15
US-09-044-718-81
: Sequence 82: Application US/09044718
: Patent No. 6391605
: GENERAL INFORMATION:
: APPLICANT: KOSTREWA, Dirk
: APPLICANT: PASAMONTES, Luis
: APPLICANT: TOMSCHY, Andrea
: APPLICANT: van LOON, Adolphus
: APPLICANT: VOGEL, Kurt
: APPLICANT: WYSS, Markus
: TITLE OF INVENTION: MODIFIED PHYTASES
: FILE REFERENCE: Modified Phytases
: CURRENT APPLICATION NUMBER: US/09/044,718
: CURRENT FILING DATE: 1998-03-19
: PRIOR APPLICATION NUMBER: EP 97810175.6
: PRIOR FILING DATE: 1997-03-25
: NUMBER OF SEQ ID NOS: 82
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 81
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
US-09-044-718-81

Alignment Scores:
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 Score: 1890.00 Matches: 358
 Percent Similarity: 84.80% Conservative: 38
 Best Local Similarity: 76.66% Mismatches: 69
 Query Match: 74.85% Indels: 2
 DB: 4 Gaps: 2

US-09-488-265B-25 (1-1426) x US-09-044-718-81 (1-465)

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

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(without alignments)
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Total number of hits satisfying chosen parameters: 1175306

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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ALIGNMENTS

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; Sequence 9, Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083.452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/09/273,871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080,129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090,675
; PRIOR FILING DATE: 1998-06-25

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Sequence 8, Appli
Sequence 78, Appl
Sequence 6, Appli
Sequence 24, Appl
Sequence 80, Appl
Sequence 79, Appl
Sequence 3, Appl
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: SOFTWARE: FastSeq for Windows Version: 4.0
: SEQ ID NO 9
: LENGTH: 467
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Variation
US-10-083-452-9

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Score: 211.00 Matches: 435
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Query Match: 91.52% Indels: 0
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: Publication No.: US20020127218A1
: GENERAL INFORMATION:
: APPLICANT: Svendsen, Allan
: TITLE OF INVENTION: Phytase Variants
: FILE REFERENCE: 5618,500-US
: CURRENT APPLICATION NUMBER: US/10/063,452
: CURRENT FILING DATE: 2002-02-26
: PRIOR APPLICATION NUMBER: US/09/273,871
: PRIOR FILING DATE: 1999-03-22
: PRIOR APPLICATION NUMBER: PA 1998 00407
: PRIOR FILING DATE: 1998-03-23
: PRIOR APPLICATION NUMBER: PA 1998 00806
: PRIOR FILING DATE: 1998-06-19
: PRIOR APPLICATION NUMBER: PA 1998 01176
: PRIOR FILING DATE: 1998-09-18
: PRIOR APPLICATION NUMBER: PA 1999 00091
: PRIOR FILING DATE: 1999-01-22
: PRIOR APPLICATION NUMBER: 60/080,129
: PRIOR FILING DATE: 1998-03-31
: PRIOR APPLICATION NUMBER: 60/090,675
: PRIOR FILING DATE: 1998-06-25
: NUMBER OF SEQ ID NOS: 15
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 465
: TYPE: PRT
: ORGANISM: Aspergillus fumigatus
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US-10-083-452-8

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DB: 14 Gaps: 2

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RESULT 3

US-10-062-848-78
Sequence 78, Application US/10062848
Publication No. US20030092155A1
GENERAL INFORMATION:
APPLICANT: KOSTREWA, Dirk
APPLICANT: PASAMONTES, Luis
APPLICANT: TOMSCHY, Andrea
APPLICANT: van LOON, Adolphus
APPLICANT: VOGEL, Kurt
APPLICANT: WYSS, Markus
TITLE OF INVENTION: MODIFIED PHYTASES
FILE REFERENCE: Modified Phytases
CURRENT APPLICATION NUMBER: US/10/062,848
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 09/044,718
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: EP 97810175.6
NUMBER OF SEQ ID NOS: 82
SOFTWARE: PatentIn ver. 2.1
SEQ ID NO 78
LENGTH: 465
TYPE: PRT
ORGANISM: Aspergillus fumigatus
US-10-062-848-78
Alignment Scores:
Pred. No.: 2,46e-145 Length: 465
Score: 1902.00 Matches: 360
Percent Similarity: 85.01% Conservative: 37
Best Local Similarity: 77.09% Mismatches: 68
Query Match: 75.33% Indels: 2
DB: 15 Gaps: 2
US-09-488-265B-25 (1-1426) x US-10-062-848-78 (1-465)

QY 12 ATGGCGGTGTCCTCGTGTACTGTCATTCGACCTGTCGCTGTCACATCCGSGTACC 71

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Db 1 MetValThrLeuThrPheLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 72 GCCTGGGCTCGTGGTAAATCTCAGCTCTGTGACACTGTGTGACGGGTGTTACCAATGT 131
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyArgGlnCys 39
QY 132 TTCACGAAATTTCTCAGTCTGGGGTCAATACTCTCCATTTCTCTCTTGGCGAGCAA 131
Db 40 SerProAlaThrSerHisLeuTyrGlyGlnTyrSerProPhePheSerLeuGluAspGln 59
QY 192 TCTGCTATTCTCCACACTTCCAAAGGTTGTACAGTTCCTTCTGCTCAAGTTCTCTC 251
Db 60 LeuSerValSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 252 AGACAGGCTGCTAGATACCAACTTCTTCTAAGTCTAAGAGTACTCTGCTTTGATTGAA 312
Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLeuValThr 99
QY 312 GCTATTCCAAAGAACCTTACGCTTTCAGGGTAAGTACGCTTCTTCAAGACTTCAAC 371
Db 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 372 TACACTTTGGGTGCTGACGACTTGACTTCCATTCGGTGAACAAATGTTAACTCTGGT 431
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnLeuValAspSerGly 139
QY 432 ATTAACTTCTACAGAGATACAGGCTTTGGCTAGAAAGATGTTCCTATTGTTAGACT 491
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValProPheIleArgAla 159
QY 492 TCTGGTCTCAGACAGATTATTGCTCTGCTGAAAGTTCATTGAAGGTTTCCAACTCTCT 551
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAla 179
QY 552 AAGTTGCTACCCAGGCTTAACTCCACACACAGCTCTCCAGTTATTAACTATTATT 611
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
QY 612 CCAAGAGTCTGCTGTACACACACACTTTGGACCCAGGTTTGTGCTACTGCTTCAAGAA 671
Db 199 ProGlnSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGlnAla 218
QY 672 TCTGAATTTGGTGACGACGTTGAAGCTAATCTCAGCTGTGTTTCCCTCCACCTATTAGA 731
Db 219 SerGlnLeuGlyAspGluAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 732 GCTAGATTGGAAGCTCACTTCCAGGTTTAACTTGACTGACCAAGAGCTTGTAACTTG 791
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 258
QY 792 ATGCACATGTCCATTCGACACTGTGTGAGAACTCTCTGACGCTACTCAATGTCGCA 851
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 279
QY 852 TCTGCTGACTTGTCTACTCAGCAAGTATTCATCAATGACTTCAATCTTGGGT 911
Db 279 PheCysGlnLeuPheThrHisAsnGluTyrLysTyrAsnTyrLeuGlnSerLeuGly 298
QY 912 AAGTACTACGTTACGGTGTGTATCCCATTCGGTCCAGCTCAAGGTGTTGGTTTCTGT 971
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 972 AACGAATTGATTGTAGATTGACTCTCTCCAGTTCAGAGACACACTTCTACTAACCAC 1031
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1032 ACTTTGACTCTATCCACGCTACTTTCCCATTTGAACGCTACTTTGTACGCTGACTTCTCT 1091
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1092 CACCACACACTATGTTTCTATTCTTCTCGCTTTCGGTTTGTACACCGCTACTAAGCA 1151
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359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
QY 1152 TTGTTTACTTACTTCTGTTGAATCTTGAAGAAATGACGATGACGCTTCTTCTGACT 1211
Db 379 LeuSerArgThrSerValGlnSerAlaLysGluLeuAspGlyTyrSerAlaSerTyrVal 398
QY 1212 GTTCCATTCGGTCTGACGCTTACGCTTGAATGATGCAATCTGAAGCTGAAGCAACCA 1271
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
QY 1272 TTGGTTAGAGTTTTCGTTAACGACAGAGCTTCTTCATTCGACGCTTCTGCTGACAAG 1331
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY 1332 TTGGTGTAGTAGTAAAGAGACGACTTCTGTTGAAGGTTTGTCTTTCGCTAGACTGGT 1391
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTyrAlaArgSerGlyGly 458
QY 1392 AACTGGGAAGAAATGTTTCGCT 1412
Db 459 AsnTyrGlyGluCysPheSer 465

RESUL 4
US-10-229-358-6
: Sequence 6, Application US/10229358
: Publication No. US20030124700A1
: GENERAL INFORMATION:
: APPLICANT: Stafford, Christian F.
: APPLICANT: Brookman, Jayne L.
: TITLE OF INVENTION: Phytase Enzymes, Nucleic Acids Encoding
: FILE OF INVENTION: Phytase Enzymes and Vectors and Host Cells Incorporating San
: FILE REFERENCE: GC586-2
: CURRENT APPLICATION NUMBER: US/10/229,358
: CURRENT FILING DATE: 2002-08-26
: PRIOR APPLICATION NUMBER: US 60/148,960
: PRIOR FILING DATE: 1999-08-13
: NUMBER OF SEQ ID NOS: 34
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 6
: LENGTH: 465
: TYPE: PRF
: ORGANISM: Aspergillus fumigatus
US-10-229-358-6

Alignment Scores:
Pred. No.: 2,46e-145 Length: 465
Score: 1902.00 Matches: 360
Percent Similarity: 85.01% Conservative: 37
Best Local Similarity: 77.09% Mismatches: 68
Query Match: 75.33% Indels: 2
DB: 15 Gaps: 2

US-09-488-265b-25 (1-1426) x US-10-229-358-6 (1-465)
QY 12 ATGGGGGTGCTGCTGCTGCTACTGTCTACTGTCCATTCGCCACTTGTTCGTTCCACATCGGTACC 71
Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 72 GCCTTGGGTCCTCGTGGTAAATCTCAGCTCTGTGACACTGTGTGACGTTGGTITACCAATGT 131
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 132 TTCACGAAATTTCTCAGTCTGGGGTCAATACTCTCCATTTCTCTCTTGGCGAGCAA 191
Db 40 SerProAlaThrSerHisLeuTyrGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY 192 TCTGCTATTCTCCACAGCTTCCAAAGGTTGTAGAGTTACTTCTGCTCAAGTTTCTCTCT 251
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 252 AGACAGGTCCTAGATACCAACTTCTTCTAAGTCTAAGAGTACTCTGCTTTGATTGAA 311
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Db 80 ArgHisGlyAlaArgTyrProThrSerSerLysLysTyrLysLysLeuValThr 39
QY 312 GCTATTCAAAACAGCGTACTGCTTTCAGAGGTAAAGTACCGCTTCTTGAGAGCTTACAAC 371
Db 100 AlalLeuGlnAlaAsnAlaThrAspPheGlyLysPheAlaPheLeuLysThrTyrAsn 119
QY 372 TACACTTTGGTGGTGCAGGACTTCACCTCCATTCGGTGAACAACAATGGTTAACTCTGGT 431
Db 120 TyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnGlnLeuValAsnSerGly 139
QY 432 ATTAGTTCTACAGAAGATACAAGGCTTTGGCTAGAGAAGATTCTCATTCGTACAGCT 491
Db 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 492 TCTGGTCTTCACAGAGTTATTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 551
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnAla 179
QY 552 AAGTGGCTGACCCAGGTGCTAACCCACACAGCTTCACAGTTCACAGTTCATTAAT 611
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 596
QY 612 CCAGAGCTGCTGTTACACACACACTTCGACACAGCTTGTGTACTGCTGCTGCTGCTGCTGCT 671
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 219
QY 672 TCTGAATTCGGTGACGAGCTTGAAGCTTAACCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
Db 219 SerGlnLeuLysAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 732 GCTAGATTGGAAGTCACTTCCAGGCTTAACTTGACAGGACGCTGCTGCTGCTGCTGCTGCT 791
Db 239 AlaArgAlaGluLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 256
QY 792 ATGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 851
Db 259 MetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGlnLeuSerPro 275
QY 852 TTCTGTGACTTGTCTCACTCAGCAGCAATGATTCATACGACTACTTGCATCTTGGGT 911
Db 279 PheCysGlnLeuPheThrHisAsnGluTrpLysLysTyrAsnTyrLeuGlnSerLeuGly 298
QY 912 AAGTACTACGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 971
Db 299 LysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIleGlyPheThr 318
QY 972 AACGAATTGATTGCTAGATTGACTCACTCTCCAGTTCACAGCAGCAGCTTCTACTAACCCAC 1031
Db 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 336
QY 1032 ACTTTGGACTTACCCAGCTACTTCCCATTTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1091
Db 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1092 CACGACACACTATGTTTCTATTTCTCTGCTTGGGTGTTGTACAACGCTACTTAAGCCA 1151
Db 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
QY 1152 TTGCTACTACTTCTGTTGAATCATTTGAAGAACTGACGGTACGCTGCTGCTGCTGCTGCTGCT 1211
Db 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
QY 1212 GTTCCATTGCTGCTAGAGCTTACGTTGAATGATGCAATGTGAGCTGAAAGGACCA 1271
Db 399 ValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
QY 1272 TTGGTAGAGTTTGGTTAAGCAGAGAGTGTTCATTTGACGCTTGGTGTGCTGCTGCTGCTGCT 1331
Db 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY 1332 TTGGTAGATGTAAGACAGAGCTTCTGTTGAAGGTTTGTCTTTCGCTAGATCTGCTGGT 1391
Db 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
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QY 1392 AACTGGGAAGAAATGTTTCGCT 1412
Db 459 AsnTrpGlyGluCysPheSer 465

RESULT 5
US-10-213-990-24
: Sequence 24, Application US/10213990
: Publication No. US20030082595A1
: GENERAL INFORMATION:
: APPLICANT: Jiang, Bo
: APPLICANT: Bussey, Howard
: APPLICANT: Storms, Reg
: APPLICANT: Roemer, Terry
: TITLE OF INVENTION: NUCLEIC ACIDS OF ASPERGILLUS FUMIGATUS ENCODING INDUSTRIAL
: FILE REFERENCE: 10182-019-999
: CURRENT APPLICATION NUMBER: US/10/213-990
: CURRENT FILING DATE: 2002-08-05
: NUMBER OF SEQ ID NOS: 72
: SOFTWARE: FastSeq for Windows Version: 4.0
: SEQ ID NO 24
: LENGTH: 474
: TYPE: PRT
: ORGANISM: Aspergillus
US-10-213-990-24

Alignment Scores:
Prod. No.: 4.76e-145 Length: 474
Score: 1898.50 Matches: 357
Percent Similarity: 84.89% Conservative: 42
Best Local Similarity: 75.95% Mismatches: 64
Query Match: 75.19% Indels: 7
DB: 15 Gaps: 2

US-09-488-265b-25 (1-1426) x US-10-213-990-24 (1-474)
QY 3 TATGAATTCATGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 62
Db 12 TyrLeuLeuSerGlyAlaValValLeuIleLeuLysArgSerArgValSerAlaAlaPro 31
QY 63 TCCGCTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 122
Db 32 SerSer-----AlaGlySerLysSerLysSerCysAspThrValAspLeuGly 45
QY 123 TACCAATGTTTCCCAAGAAATTCCTCACTTGTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 182
Db 46 TyrGlnCysSerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeu 65
QY 183 GCTGACGAATCTGCTATTTCTCCAGAGCTTCCAAAGGTTGTAGAGTTACTTTCGTTCAA 242
Db 66 GluAspGluLeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGln 85
QY 243 GTTGTGCTAGACACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
Db 86 ValLeuSerArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLys 105
QY 303 TTGATTGAAGCTATTCAAAGACGCTGCTGCTTTCAGGGTAAGTACGCTTCTTGAAG 362
Db 186 LeuValThrAlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLys 125
QY 363 ACTTACACTACACTTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
Db 126 ThrTyrAsnTyrThrLeuGlyAlaAspLeuThrProPheGlyGluGlnLeuVal 145
QY 423 AACTCTGTTATTAAGTTCTACAGAAGATACAAGGCTTGGCTTGAAGAGTTGTTCCATTC 482
Db 146 AsnSerGlyIleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPhe 165
QY 483 GTTAGAGCTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
Db 166 IleArgAlaSerGlySerAspArgValIleAlaSerGlyLysPheIleGluGlyPhe 185
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QY 543 CAATCTGCTAAGTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAC 602
Db 186 GlnAlaLysLeuAlaAspProGlyAlaThr ---AsnArgAlaAlaProAlaIleSer 204
QY 603 GTTATTATCCGAAGGIGCTGTTTCAACAACACACTTGGACACCGTTTGTGTATGCT 462
Db 205 ValIleIleProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLys 224
QY 563 TTCGAAGATCTGAATTCGGTGACGAGGTGAAGCTAACTTACCTGCTGCTTTTCGCTCA 722
Db 225 PheGluAlaSerGlnLeuGlyAspGluValAlaAlaAsnThrAlaLeuPheAlaPro 244
QY 723 CCTATTAGACTAGATTGGAAGCTACCTGCCAGGTGTTAACTTACTGACACCAAGACGTT 782
Db 245 AspIleArgAlaArgAglLysHisLeuProGlyValThrLeuThrAspLysVal 264
QY 783 GTTAACCTGATGACATGTGTCATTCGACACTGTGTGAGAACTTTCGACCTACTCAA 842
Db 265 ValSerLeuMetAspMetCysSerPheAspThrValAlaArgThrSerAspAlaSerGln 284
QY 843 TTGTCTCCATCTGTGACTTCTTCACTCAGCAGGANTGATTCATACGACTACTTGCAG 902
Db 285 LeuSerProPheCysGlnLeuPheThrHsasngluTrpLysLysThrAsnThrLeuGln 304
QY 903 ICTTTGGGTAACTACGCTTACGGTGTGTTACCCATTCGGTCCAGCTCAAGGTGT 962
Db 305 SerLeuGlyLysTyrrGlyTyrrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIle 324
QY 963 GGTTCGTTAACCAATGTGTTAGATTGACTCACTCTCCAGTTCAAGACCACTTCT 1022
Db 325 GlyPheThrAsnGlnLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSer 344
QY 1023 ACTAACCACTTTGACCTTAACCCAGCTACTTTCCTCCATTTGAAGCTACTTGTACGCT 1082
Db 345 ThrAsnSerThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrrVal 364
QY 1083 GACTCTCTCACCACACACACTGTTCTTCTATTCTTCTCGCTTTGGGTTGTACACGGT 1142
Db 365 AspPheSerHisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrrAsnGly 384
QY 1143 ACTAAGCATTTGCTACTACTTCTGTGATCTATTGGAAGAACTGACGGTTACGCTGT 1202
Db 385 ThrGluProLeuSerArgThrServalGluSerAlaLysGluLeuAspGlyTyrrSerAla 404
QY 1203 TCTTGGACTGTTCCATTCGCTGCTAGAGTTAGCTTGAATGATGCAATGTGAAGCTGAA 1262
Db 405 SerTrpValValProPheGlyAlaArgAlaTyrrPheGluThrMetGlnCysLysSerGlu 424
QY 1263 AAGGAACCATTTGATAGAGTTTGGTTAAGCAGAGAGTTGTTCCATTCGACGGTTGTGGT 1322
Db 425 LysGluProLeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAsp 444
QY 1323 GTTGCAAGTTGGGTACATGTAAAGAGACGACTTGGTTGAAGGTTGTGCTTTCGCTAGA 1382
Db 445 ValAspLysLeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArg 464
QY 1383 TCTGGTGGTAACTGGGAAGAACTTTCGCT 1412
Db 465 SerGlyGlyAsnTrpGlyGluCysPheSer 474
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RESULT 6

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US-10-062-848-80
; Sequence 80, Application US/10062848
; Publication No. US20030092155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTRENA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
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; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
; US-10-062-848-80

Alignment Scores:
Pred. No.: 1,09e+144 Length: 465
Score: 1894.00 Matches: 359
Percent Similarity: 84.80% Conservative: 37
Best Local Similarity: 76.87% Mismatches: 69
Query Match: 75.01% Indels: 2
Db: 15 Gaps: 2
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US-09-488-265b-25 (1-1426) x US-10-062-848-80 (1-465)

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QY 12 ATGGCGCTGTTGCTGCTGCTACTGTCATGTCACCTGTCGTTCCGTTCCACATCCGTAAC 71
Db 1 MetValThrLeuThrPheLeuLeuSerAlaAlaTyrLeuLeuSerGlyArgValSerAla 20
QY 72 GCCTTGGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 131
Db 21 AlaProSerSerAlaGly---SerLysSerCysAspThrValAspLeuGlyTyrrGlnCys 39
QY 132 TTCACGAAATTTCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 191
Db 40 SerProAlaThrSerHisLeuTrpGlyGlnTyrSerProPhePheSerLeuGluAspGlu 59
QY 192 TCTGCTATTCTCCAGACGCTCCAAAGGCTGTAGAGTTACTTCTGCTCAAGTTTGTCT 251
Db 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 252 AGACAGGCTCAGATACCACTTCTTCAAGTCTAAGCTCTAAGACTACTCTGCTTGTGATA 311
Db 80 ArgHisGlyAlaArgIleProThrSerSerLysSerLysLysLysLysLysLysLysLys 99
QY 312 GCTATTCAAAGAACCTACTGCTTCAAAGGCTAAGTAGCTTCTTCTGAAGACTTACAAAC 371
Db 100 AlalleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrTyrrAsp 119
QY 372 TACACTTGGTCTCAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 431
Db 120 TyrThrLeuGlyAlaAspAspLeuThrProPheGlyGlnGlnGlnLeuValAsnSerGly 139
QY 432 ATTAAGTTCTACAGAATACAGAGCTTTGGCTAGAAAGATTTGCTTCCATTCCTAGAGCT 491
Db 140 IleLysPheTyrrGlnArgTyrrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 492 TCTGGTCTGACAGAGATTATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 551
Db 160 SerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPheGlnGlnAla 179
QY 552 AAGTTGGCTGACCCAGGTGCTAACCCACACCAAGCTTCTCCAGTTATTAAAGCTTATTATT 611
Db 180 LysLeuAlaAspProGlyAlaThr---AsnArgAlaAlaProAlaIleSerValIleIle 198
QY 612 CCAGAAGGCTGCTGTTTACAAACACACTTTGGACACGAGGTTTGTGTACTGCTGCTTCAAGAA 671
Db 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 218
QY 672 TCTGAATTTGGTGCACCGCTGACCTTAACCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 731
Db 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 732 GCTAGATTGGAAGCTCACTTGCAGGTGTTAACTTGAAGTCTGCTGCTGCTGCTGCTGCTGCT 791
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; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Aspergillus fumigatus
US-10-062-848-81

Alignment Scores:
Pred. No.: 2 3e-144 Length: 465
Score: 1890.00 Matches: 358
Percent Similarity: 84.80% Conservative: 38
Best Local Similarity: 76.66% Mismatches: 69
Query Match: 74.85% Indels: 2
DB: 15 Gaps: 2

US-09-488-265b-25 (1-1426) x US-10-062-848-81 (1-465)

QY 12 ATGGGGGTGTCGTCGTGTCAGTCCATTCGCACCTGTCGTTCCACATCCCGGTACC 72
DB 1 MetValThrLeuThrPheLeuLeuSerAlaAlaLysLeuLeuSerGlyArgValSerAla 20
QY 72 GCCTTGGGTCCTCGTGAATCTCTCACTCTTGACACTGTTGACGGTGGTTACCAAGT 131
DB 21 AlaProSerSerAlaGly--SerLysSerCysAspThrValAspLeuGlyTyrGlnCys 39
QY 132 TTCGCCAAMATTCTCAGCTGTGGGTCAATCTCTCCATCTTCTCTTGGCTGACCAA 191
DB 40 SerProAlaThrSerHisLeuTyrGlyGlnTyrSerProPheSerLeuGluAspGlu 59
QY 192 TCTGCTATTCTCCACAGCTTCCAAAGGTTCTAGAGTTACTTCTTCAAGTTTGTCT 251
DB 60 LeuSerValSerSerLysLeuProLysAspCysArgIleThrLeuValGlnValLeuSer 79
QY 252 AGACAGGCTAGATACCCACACTCTCTTAAGTCTAAGAGTACTGCTTGTATGAA 312
DB 80 ArgHisGlyAlaArgTyrProThrSerSerLysSerLysLysTyrLysLysLeuValThr 99
QY 312 GCTATTCAAAGAACGCTACTGCTTTCAAGGTTAAGTACGCTTCTTGAAGACTTACAG 371
DB 100 AlaIleGlnAlaAsnAlaThrAspPheLysGlyLysPheAlaPheLeuLysThrLysAsn 119
QY 372 TACACTTTGGGTCTCAGCACTTGACTCCATTCGGTGAACACAAATGGTTAACTCTGT 431
DB 120 TyrThrLeuGlyAlaAspLeuThrAlaPheGlyGlyGlnGlnLeuValAsnSerGly 139
QY 432 ATTAAGTCTTACACACATACAGCGCTTGGCTAGAAAGATTCTCCATCTCTAGACT 491
DB 140 IleLysPheTyrGlnArgTyrLysAlaLeuAlaArgSerValValProPheIleArgAla 159
QY 492 TCTGGTTCTGACAGAGTTATGCTTCTGCTGAAAGTTTCATTGAAGGTTTCCAACTGCT 551
DB 160 SerGlySerAspArgValIleAlaSerGlyGlyLysPheIleGluGlyPheGlnGlnAla 179
QY 552 AGTTGCTGCTACCCAGTCTTAACCCACACAGCTTCTCCAGTTATTAACGTTATATT 611
DB 180 LysLeuAlaAspProGlyAlaThr--AsnArgAlaAlaProAlaIleSerValIleIle 198
QY 612 CCAGAGGCTGCTGGTTACACACACTTGGACCGGTTTCTGTACTGCTTCTTCAGAA 672
DB 199 ProGluSerGluThrPheAsnAsnThrLeuAspHisGlyValCysThrLysPheGluAla 216

672 ICTGAATTGGTGACAGACGTTGAAGCTAACTTCACTGCTGCTTTTCGCTCCACCTATTAGA 731
DB 219 SerGlnLeuGlyAspGluValAlaAlaAsnPheThrAlaLeuPheAlaProAspIleArg 238
QY 732 GCTAGATTGGAAGCTCACTGCCAGGTGTTAACTTGAAGTGAAGAGCGTTGTAACCTG 791
DB 239 AlaArgAlaLysLysHisLeuProGlyValThrLeuThrAspGluAspValValSerLeu 259
QY 792 ATGACATGTGTCATTCGACACTGTGTAGAACTTCTGACGCTACTCAATTTGCTCCA 851
DB 259 MetAspMetCysSerPheAspThrValAlaAlaArgThrSerAspAlaSerGlnLeuSerPro 278
QY 852 TCTGTGACTTGTCTCACTCAGCAGCAATGGATTCAATAGSACTACTTGCATCTTGGGT 911
DB 279 PheCysGlnLeuPheThrHisAsnGlnLysLysLysLysLysLysLysLysLysLys 298
QY 912 AAGTACTACGGTTACGGTGTGTAACCCATTCACCATTTGGGTGCGAGCTCAAGGTGTTGGT 971
DB 299 LysTyrTyrGlyTyrGlyValAlaGlyAsnProLeuGlyProAlaGlnGlyLysGlyPheThr 318
QY 972 AACGAATTGATTGCTAGATTGACTCTCTCCAGTTCAGACACACTTCTACTAACCA 1031
DB 319 AsnGluLeuIleAlaArgLeuThrArgSerProValGlnAspHisThrSerThrAsnSer 338
QY 1032 ACTTTGGACTCTAACCCAGCTACTTCCCATTTGAACGCTACTTGTAGCGTACTCTCT 1091
DB 339 ThrLeuValSerAsnProAlaThrPheProLeuAsnAlaThrMetTyrValAspPheSer 358
QY 1092 CAGCACAACACTATGCTTCTATTTTCTTGGCTTTGGGTGTTGTACAGCGTACTAACCA 1151
DB 359 HisAspAsnSerMetValSerIlePhePheAlaLeuGlyLeuTyrAsnGlyThrGluPro 378
QY 1152 TTCTCTACTACTTCTGTTCAATCTATTGAAGAACTGACGGTTCAGCTGCTTCTTGGACT 1211
DB 379 LeuSerArgThrSerValGluSerAlaLysGluLeuAspGlyTyrSerAlaSerTrpVal 398
QY 1212 GTTCATTCCTGCTAGAGCTTACGTTGAAATGATGCAATGTAAGTGAAGCTGAAAGAACCA 1271
DB 399 ValProPheLeuAlaArgAlaTyrPheGluThrMetGlnCysLysSerGluLysGluPro 418
QY 1272 TTGGTTAGACTTTGGTTAACGACAGGTTTCCATTCACGGTGTGGTGTGTCACAA 1331
DB 419 LeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAspValAspLys 438
QY 1332 TTGGGTAGATGTAAGAGACGACTTTCGTTGAAGGTTTGTCTTTCGCTAGATCTGGTGT 1391
DB 439 LeuGlyArgCysLysLeuAsnAspPheValLysGlyLeuSerTrpAlaArgSerGlyGly 458
QY 1392 AACTGGGAAGATGTTTCGCT 1412
DB 459 AsnTrpGlyGluCysPheSer 465

RESULT 1:
US-10-062-848-82
; Sequence 82, Application US/10062848
; Publication No. US20030052155A1
; GENERAL INFORMATION:
; APPLICANT: KOSTREWA, Dirk
; APPLICANT: PASAMONTES, Luis
; APPLICANT: TOMSCHY, Andrea
; APPLICANT: van LOON, Adolphus
; APPLICANT: VOGEL, Kurt
; APPLICANT: WYSS, Markus
; TITLE OF INVENTION: MODIFIED PHYTASES
; FILE REFERENCE: Modified Phytases
; CURRENT APPLICATION NUMBER: US/10/062,848
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 09/044,718
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: EP 97810175.6
; PRIOR FILING DATE: 1997-03-25
; NUMBER OF SEQ ID NOS: 82
; SOFTWARE: PatentIn Ver. 2.1
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/ SEQ ID NO 82

/ LENGTH: 469

/ TYPE: PRT

/ ORGANISM: Aspergillus fumigatus

US-10-062-848-82

Alignment Scores:

Pred. No.: 1,39e-142 Length: 469
Score: 1868.00 Matches: 348
Percent Similarity: 85.11% Conservative: 52
Best Local Similarity: 74.04% Mismatches: 66
Query Match: 73.98% Indels: 4
DB: 15 Gaps: 2

US-09-488-265B-25 (1-1426) x US-10-062-848-82 (1-469)

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DB 1 MetGlyAlaLeuThrPheLeuLeuSerValMetTyrLeuLeuSerGlyValAlaGlyAla 20
QY 69 -----ACCGCGTTCGGTGGTGGTAAATTCACATCTGTGACACTGTGACGGTGT 122
DB 21 ProSerSerGlyCysSerAlaGlySerGlySerLysAlaCysAspThrValGluLeuGly 40
QY 123 TACCAATGTTCCACAGAAATTCCTCACTTGTGGGTCAATACACTCTCCTCTCTCTG 182
DB 41 TyrGlnCysSerProGlyThrSerHisLeuTyrGlyGlnTyrSerProPheSerLeu 60
QY 183 GCTGACGAACTGCTATTTCGCCAGAGCTTCCAAAGGGTGTAGACTTACTTCGCTCAA 242
DB 61 GluAspGluLeuSerValSerSerAspLeuProLysAspCysArgValThrPheValGln 60
QY 243 GTTTGTGTACACAGCTGTAGATACCAACTCTCTTAAGTCTAAGAGTACTCTGCT 302
DB 81 ValLeuSerArgHisGlyAlaArgTyrProThrAlaSerLysSerLysLysLysLys 100
QY 303 TTGATTGAAGTATTCAAAAGACGCTACTGCTTCAAGGCTAAGTACGCTTCTTGAAG 362
DB 101 LeuValThrAlaLeuGlnLysAsnAlaThrGluPheLysGlyLysPheAlaPheLeuGlu 120
QY 363 ACTTACAACTACATTTGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 422
DB 121 ThrTyrAsnTyrThrLeuGlyAlaAspAspLeuThrProPheGluGlnGlnMetVal 40
QY 423 AACTCTGTTAATAGTCTACAGAGATACAGGCTTGGCTAGAGATGTCATTC 482
DB 141 AsnSerGlyLeuLysPheTyrGlnLysTyrLysAlaLeuAlaGlySerValValProPhe 160
QY 483 GTTAGAGCTTCTGGTCTGACAGAGTATTGCTCTCTGCTGAAAGTTCATTAAGTTTC 542
DB 161 IleArgSerSerGlySerAspArgValIleAlaSerGlyGluLysPheIleGluGlyPhe 180
QY 543 CAATCTGTAACTGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 602
DB 181 GlnGlnAlaAsnValAlaAspProGlyAlaThr---AsnArgAlaAlaProValIleSer 199
QY 603 GTTATTATTCAGAGGTCGTGGTTACACACACTTTGGACACCGTGTGTGTACTGCT 662
DB 200 ValIleIleProGluSerGluThrTyrAsnAsnThrLeuAspHisSerValCysIleAsn 219
QY 663 TTCGAAGAATCTGAATTTGGGTGACGAGTTCAGCTAATCTCACTGCTGTTTTCGCTCA 722
DB 220 PheGluAlaSerGluLeuGlyAspGluValGluAlaAsnPheThrAlaLeuPheAlaPro 239
QY 723 CCTATTAGAGCTAGATTGGAAGCTCACTTGCAGGTGTTAACTTGACTGACGAGACGTT 782
DB 240 AlaIleArgAlaArgIleGluLysHisLeuProGlyValGlnLeuThrAspAspVal 259
QY 783 GTTAACCTTGATGACATGCTGCCATTCGACACTGTCGACACTTCTGACGCTACTCAA 842
DB 260 ValSerLeuMetAspMetCysSerPheAspThrValAlaArgThrAlaAspAlaSerGlu 279
QY 843 TTGCTCCATCTGTGACTTGTTCACCTACGACGAAATGGATTCAATACGACTACTTCCAA 902
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DB 280 LeuSerProPheCysAlaIlePheThrHisAsnGluTyrLysLysTyrAspTyrLeuGln 299
QY 903 TCTTTGGTAACTACTACGCTTACGGTGGTAAACCCATTTGGTGGTGGTGGTGGTGGT 962
DB 300 SerLeuGlyLysTyrTyrGlyTyrGlyAlaGlyAsnProLeuGlyProAlaGlnGlyIle 319
QY 963 GGTTCGTTAACGAATGATTGCTAGATTGACTCACTCTCCACTTCCACTTCAAGCACACTTCT 1022
DB 320 GlyPheThrAsnGluLeuIleAlaArgLeuThrAsnSerProValGlnAspHisThrSer 339
QY 1023 ACTAACACACTTTGGACTCTAACCCAGCTACTTCCCATTTGACACCTTACTTTGTACGCT 1082
DB 340 ThrAsnSerThrLeuAspSerAspProAlaThrPheProLeuAsnAlaThrIleTyrVal 359
QY 1053 GACTCTCTCACCACAAACACTATGGTTCATTTCTTCTTCTGCTTGGTGGTGGTGGTGGT 1142
DB 360 AspPheSerHisAspAsnGlyMetIleProIlePhePheAlaMetGlyLeuTyrAsnGly 379
QY 1143 ACTAAGCATTTGCTACTTCTCTGTTGAATCTTATTAAGAACTTCAAGAACTTCAAGCTGCT 1202
DB 380 ThrGluProLeuSerGlnThrSerGluGluSerThrLysGluSerAsnGlyTyrSerAla 399
QY 1203 TCTTGGACTGTTCCATTCGCTGCTAGAGCTTACGTTGCAATGTCATGTCGAACTGAA 1262
DB 400 SerTyrAlaValProPheGlyAlaArgAlaTyrPheGluThrMetGlnCysLysSerGlu 419
QY 1263 AAGAACCATTTGGTTAGAGTTTGGTTAAGCAGAGAGTTGTTCCATTCGACGCTGTTGCT 1322
DB 420 LysGluProLeuValArgAlaLeuIleAsnAspArgValValProLeuHisGlyCysAla 439
QY 1323 GTTACAGTGGGTAGATGTAAGACAGACGCTGCTGTTGAAGTTCGCTTCGCTAGA 1382
DB 440 ValAspLysLeuGlyArgCysLysLeuLysAspPheValLysGlyLeuSerTyrPalaArg 459
QY 1393 TCTGGTGGTAACTCGGAAGAATGTTTCGCT 1412
DB 450 SerGlyGlyAsnSerGluGlnSerPheSer 469
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RESULT 12

US-10-079-709-32

/ Sequence 32, Application US/10079709

/ Publication No. US20030119163A1

GENERAL INFORMATION:

/ APPLICANT: Robert F.M. Van Gorcom
/ APPLICANT: Willem Van Hartingsveldt
/ APPLICANT: Petrus A. Van Paridon
/ APPLICANT: Annemarie E. Veenstra
/ APPLICANT: Rudolf G.M. Luttin
/ APPLICANT: Gerardus Selten
/ TITLE OF INVENTION: Cloning and Expression of Microbial
/ TITLE OF INVENTION: Phytase
/ NUMBER OF SEQUENCES: 52
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Morrison & Foerster
/ STREET: 545 Middlefield Road, Suite 200
/ CITY: Menlo Park
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94025-3471
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ SOFTWARE:
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/079,709
/ FILING DATE: 02-FEB-2002
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/233,510
/ FILING DATE: 20-JAN-1999

DD LYSIYIYIGLNIISGLYATAAGLYASNPITOLENGLYPIOTIHG-GHGLYVAIGLYIYATA 320

QY 12 ATGGGGGCTTTCGTCGTGCTACTCTCCATTCACCTTCTTCGGTTCACATCCGGTACC 71

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Db 1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20
QY 72 GCCTGGGTCCTCGTGGTAAATCTCACACTCTGTGACACIGTGTGACGGTGGTTACCAATGT 131
Db 21 AlaValProAlaSerArgAsnGlnSerThrCysAspThrValAspGlnGlyTyrGlnCys 40
QY 132 TCCACAGAAATTTCTCACACTTGGGGTCAATACTCTCCATCTCTCTCTTGGCTGACGAA 191
Db 41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnIys 60
QY 192 TCTGCTATTCTCCAGACACTTCCAAAGGGTGTGTAGAGTACTTTCGTTCAAGTTTGTCT 251
Db 61 SerAlaIleSerProAspValProAlaGlyCysHisValThrPheAlaGlnValLeuSer 60
QY 252 AGACAGGGTGCTAGATACCCAACTCTCTTAAGTCTAAGAAGTCTGCTTCATTGAA 311
Db 81 ArgHisGlyAlaArgTyrProThrAspSerLysGlyLysLysTyrSerAlaLeuIleLeu 100
QY 312 GCTATTCAAAGAAGCGTACTGCTTTCAAGGTAAGTACGGCTTTCTTGAAGACTTACAA 371
Db 101 GluIleGlnAsnAlaThrThrPheGluGlyLysTyrAlaPheLeuLysThrTyrAsn 120
QY 372 TACACTTTCGGTCTGACGACTGACTGCTCATTCGCTGACACAAAGTGTAACTTCGT 431
Db 121 TyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY 432 ATTAAGTCTACAGAGATACAAAGCTTTGGCTAGAAAGATTGTTCATTCGTTAGAGCT 491
Db 141 ValLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160
QY 492 TCTGGTCTGACAGAGTATTGCTTCTGCTGAGAAAGTTCATTGAAGGTTTCCATCTGCT 551
Db 161 SerGlySerSerArgValIleAlaSerGlyAsnLysPheIleGluGlyPheGlnSerThr 180
QY 552 AAGTTCGGCTGACAGGCTTAACCCACACCAAGCTCTCCAGTATTAACTGTTATT 611
Db 181 LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValIle 200
QY 612 CCAGAAGTGTGGTGTACAAACACTTTGGACACAGGTTGTGTACTGCTTTCGAGAA 671
Db 201 SerGluAlaSerThrSerAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY 672 TCTGAATTCGGTGACGACCTTCAAGCTTAACCTCACTGCTGTTCGCTCCACTTAAGA 731
Db 221 SerGluLeuAlaAspAspIleGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
QY 732 GCTAGATTGGAAGCTCATTGCCAGGTGTTAACTTCACTGACGACGAGCGTTGTTAACT 791
Db 241 GlnArgLeuGluAsnAspLeuSerGlyValSerLeuThrAspThrGluValThrTyrLeu 260
QY 792 ATGCACATGTGCTCCATTCACACTGCTGTAGAACTTCTGACGCTACTCAATTCTCCA 851
Db 261 MetAspMetCysSerPheAspThrIleSerThrSerIleValAspThrLysLeuSerPro 280
QY 852 TCTGTGACTGTGCTCACTCACGCAAGTATTCAAIACGACTACTTCCATCTTTCGGT 911
Db 281 PheCysAspLeuPheThrHisGluGluTrpIleAsnTyrAspTyrLeuGlnSerLeuAsn 300
QY 912 AACTACTACGGTACGGTCTGCTAAGCCANTGGCTCCAGCTCAAGGTGTTGCTTTCGT 971
Db 301 LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
QY 972 AACGAATTGATTGCTAGATTGACTCTCCACTCTCCACTCAAGACCACTCTTCACTAAC 1031
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QY 1032 ACTTTCGACTCTAACCCACTACTTCCANTTGAACGCTACTTTCACGCTGACTTCTCT 1091
Db 341 ThrLeuAspSerAsnProAlaThrPheProLeuAsnSerThrLeuTyrAlaAspPheSer 360
QY 1092 CACGCAACACTATGTTTCTATTCTTCGCTTGGTGGTTGTACAAAGCTTACTAACGCA 1151
Db 361 HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380
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RESULT 15

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US-10-083-452-11
; Sequence 11. Application US/10083452
; Publication No. US20020127218A1
; GENERAL INFORMATION:
; APPLICANT: Svendsen, Allan
; TITLE OF INVENTION: Phytase Variants
; FILE REFERENCE: 5618.500-US
; CURRENT APPLICATION NUMBER: US/10/083.452
; CURRENT FILING DATE: 2002-02-26
; PRIOR APPLICATION NUMBER: US/99/273.871
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: PA 1998 00407
; PRIOR FILING DATE: 1998-03-23
; PRIOR APPLICATION NUMBER: PA 1998 00806
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: PA 1998 01176
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: PA 1999 00091
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/080.129
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/090.675
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Aspergillus ficum
US-10-083-452-11
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Alignment Scores:

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Score: 1850.00 Matches: 346
Percent Similarity: 83.51% Conservative: 44
Best Local Similarity: 74.09% Mismatches: 77
Query Match: 73.27% Indels: 0
DB: 14 Gaps: 0
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US-09-488-265b-25 (1-1426) x US-10-083-452-11 (1-467);

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Db 1 MetGlyValSerAlaValLeuLeuProLeuTyrLeuLeuSerGlyValThrSerGlyLeu 20
QY 72 GCCTGGGTCCTCGTGGTAAATCTCACACTTGTGACACIGTGTGACGGTGGTTACCAATGT 131
Db 21 AlaValProAlaSerArgAsnGlnSerThrValAspGlnGlyTyrGlnCys 40
QY 132 TCCACAGAAATTTCTCACACTTGGGGTCAATACTCTCCATCTCTCTCTTGGCTGACGAA 191
Db 41 PheSerGluThrSerHisLeuTrpGlyGlnTyrAlaProPhePheSerLeuAlaAsnIys 60
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Db      41  PheSerGluThrSerHisLeuTrpGlyGlnItyrAlaProPhePheSerLeuAlaAsnGlu 60
QY      192  TCTGCTATTCTCCAGAGTTCCAAAGGGTGTAGAGTTACTTTCGTTCAAGTTCGTTGCT 251
Db      61  SerValIleSerProGluValProAlaGlyCysArgValThrPheAlaGlnValLeuSer 80
QY      252  AGACACGGTGTGTAGATACCCCAACTTCCTTAAGTCTAAGAAGTACTCTGCTTCATTGAA 311
Db      81  ArgHisGlyAlaArgItyrProThrAspSerIysGlyLysItyrSerAlaLeuIleGlu 100
QY      312  GCTATTCAAAGAACGCTACTGCTTCCTCAAGGGTAAGTACGGTTCCTTGAAGACTTACAA 371
Db      101  GluIleGlnGlnAsnAlaThrPheAspGlyLysItyrAlaPheLeuLysThrItyrAsn 120
QY      372  TACACTTTCGGTGTGACGACTTGACTCCATTCCTGCTGACCAACAAGTGGTTAACTCTGG 431
Db      121  TyrSerLeuGlyAlaAspLeuThrProPheGlyGluGlnGluLeuValAsnSerGly 140
QY      432  ATTAAGTTCTACAGAAGATACAAGGCTTTGGCTAGAAAGATTGTCCATTGCTTAGAGCT 491
Db      141  IleLysPheTyrGlnArgTyrGluSerLeuThrArgAsnIleValProPheIleArgSer 160
QY      492  TCTGCTTCGACAGAGTTATGCTTCTGCTGCTGAAAGTTCATGAAGGTTTCCATCTGCT 551
Db      161  SerGlySerArgValIleAlaSerGlyLysPheIleGluGlyPheLeuSerThr 180
QY      552  AAGTTGGGTGACCCAGGTGCTAACCCACCAAGGCTCTCCAGTTATTAACTTAATTAT 611
Db      181  LysLeuLysAspProArgAlaGlnProGlyGlnSerSerProLysIleAspValIle 200
QY      612  CCAGAAGGTGTGGTGTATACAACAACACTTTGGACCAACGGTTGTGTACTGCTTCCAA 671
Db      201  SerGluAlaSerSerSerAsnAsnThrLeuAspProGlyThrCysThrValPheGluAsp 220
QY      672  TCTGATTCGGGTGACGAGTGTGAAGTCAACTCACTGCTGTTTTCGCTCCACCTATTAGA 731
Db      221  SerGluLeuAlaAspThrValGluAlaAsnPheThrAlaThrPheValProSerIleArg 240
QY      732  GCTAGATTGGAGGCTCACTTGCCAGGTGTAACTTGACTGACGAGAGCGTTGTTAAGTIG 791
Db      241  GlnArgLeuGluAsnAspLeuSerGlyValThrLeuThrAspThrGluValThrItyrLeu 260
QY      792  ATGGACATGTGTCCATTGACACTGTTCAGACTTCTGACGCTACGCTACCAATGTCTCCA 851
Db      261  MetAspMetCysSerPheAspThrIleSerThrSerThrValAspThrLysLeuSerPro 280
QY      852  TTCTGTGCTCTTCTCACTCAGCAGCAATGGATTCAATACGACTACTTCGCAATCTTGGT 911
Db      281  PheCysAspLeuPheThrHisAspIleTrpIleAsnTyrAspTyrLeuGlnSerLeuLys 300
QY      912  AAGTACTACGGTTACGGTCTGGTAAACCATTTGGTCCAGCTCAAGGTGTGGTTTCGTT 971
Db      301  LysTyrTyrGlyHisGlyAlaGlyAsnProLeuGlyProThrGlnGlyValGlyTyrAla 320
QY      972  AACGAATTCATTGCTAGATTGACTCACTCTCCAGTTCAAGACCACACTTCTACAAACCAC 1031
Db      321  AsnGluLeuIleAlaArgLeuThrHisSerProValHisAspAspThrSerSerAsnHis 340
QY      1032  ACTTTGGACTCTAACCCAGCTACTTCCCATTTGACAGCTACTTTGTACGCTCACTTCTCT 1091
Db      341  ThrLeuAspSerSerProAlaThrPheProLeuLysSerThrLeuTyrAlaAspPheSer 360
QY      1092  CACGACACACATGTTCTTCTATTTCCTTCGCTTTGGTTTGTACAAAGGCTAAGCCA 1151
Db      361  HisAspAsnGlyIleIleSerIleLeuPheAlaLeuGlyLeuTyrAsnGlyThrLysPro 380
QY      1152  TTGCTCTACTACTTCTGTTCAATCTATTGAAGAACTGACGGTTACGCTGCTTCTTGGACT 1211
Db      381  LeuSerThrThrValGluAsnIleThrGlnThrAspGlyPheSerSerAlaIleThr 400
QY      1212  GTTCCATTCCGCTGCTAGCTTACGTTGAAATGATGCAATGTGAAGCTGAAAGCAACCA 1271
Db      401  ValProPheAlaSerArgLeuTyrValGluMetMetGlnCysGlnAlaGluGlnAlaPro 420

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QY      1272  TTGGTTAGACTTTTGGTTAACGACAGAGTTGTTCCATTCCACGGTTGTGCTGTTGACAAAG 1331
Db      421  LeuValArgValLeuValAsnAspArgValValProLeuHisGlyCysProValAspAla 440
QY      1332  TTGGGTAGATGTAAAGAGACGAGACTTTCGTTGAAGGTTTCTCTTCCGCTAGATCTGGTGGT 1391
Db      441  LeuGlyArgCysThrArgAspSerPheValArgGlyLeuSerPheAlaArgSerGlyGly 460
QY      1392  AACTGGGAAGAATGTTTCGCT 1412
Db      461  AspTrpAlaGluCysPheAla 467

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Search completed: October 3, 2003, 09:05:28
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